

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:

February 20, 2002, 20:40:31 ; Search time 1476.91 Seconds

(without alignments)
4858.978 Million cell updates/sec

Title: US-08-836-455-1

Perfect score: 435

Sequence: 1 ATGGGGCCCTGCTAGAT.....CACCATCCAGTAGCTTGGG 435

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1472140 seqs, 824859755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: qb_un:*

14: qb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_om:*

20: em_or:*

21: em_ov:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_rod:*

33: em_htg_hum:*

34: em_htg_inv:*

35: em_htg_rod:*

36: em_htg_other:*

RESULT No.	Score	Query Match	Length	DB	ID	Description
1	377	86.7	381	10	AF124721	AF124721 Mus muscu
2	117	26.9	321	10	AF163749	AF163749 Mus muscu
3	108	>24.8	303	10	MUSGLAFA	055588 Mus musculu
4	107	24.6	302	10	MNU55588	021066 Mus musculu
5	100	23.0	273	10	MNU21066	M36246 Mouse Ig ka
6	100	23.0	276	6	AR026090	AR026090 Sequence
7	100	23.0	279	10	MWTRMRB11	X63811 M.musculus
8	100	23.0	283	10	AF144956	AF144956 Mus musculus
9	100	23.0	285	10	MNU29617	U29617 Mus musculu
10	100	23.0	324	6	103643	103643 Sequence 4
11	100	23.0	324	6	107835	107835 Sequence 4
12	100	23.0	381	10	AF045495	AF045495 Mus muscu
13	100	23.0	381	10	AF045508	AF045508 Mus muscu
14	100	23.0	443	10	MNU8675	U88675 Mus musculu
15	100	23.0	443	10	MUSIGKAC1	J00565 Mouse Ig ka
16	100	23.0	684	10	MUSIGK7	V00808 Part of the
17	100	23.0	685	10	MUSIKCC	L14880 Mus musculu
18	99	22.8	390	10	MNU242670	AJ242670 Mus muscu
19	97	22.3	640	10	MUSIGKCNK	M19914 Mouse Ig re
20	91	20.9	456	10	MUSIGKCNK	I32991 Sequence 45
21	90	20.7	438	6	E09035	E09035 cDNA encodi
22	90	20.7	438	22	MUSIGKAA3	M59920 Mouse Ig ge
23	89	20.5	321	10	MUSIGK	I48667 Mus musculu
24	89	20.5	324	10	MUSK	AF045510 Mus muscu
25	89	20.5	381	10	MMU0510	AF144902 Mus muscu
26	88	20.2	290	10	AF144902	Mus musculu
27	86	19.8	308	10	AF139248	AF139248 Mus muscu
28	86	19.8	618	10	MUSIGLAPA	D29668 Mouse mRNA
29	85	19.5	423	10	MNU39902	U39902 Mus musculu
30	85	19.5	438	10	MNU39903	U39903 Mus musculu
31	85	19.5	471	10	MMU24115	U24115 Mus musculu
32	85	19.5	593	10	MMGCM65A	X57856 M.musculus
33	85	19.5	642	6	AR030520	AR030520 Sequence
34	85	19.5	642	6	AR105241	AR105241 Sequence
35	85	19.5	642	10	MNU28969	U28969 Mus musculu
36	85	19.5	681	10	MNU936L	Z48768 M.musculus
37	85	19.5	681	10	MMTGK9	V00810 M.musculus
38	85	19.5	943	10	MUSIGKAJ	J00560 mouse ig ka
39	85	19.5	1101	10	MNU68543	U68543 Mus musculu
40	84	19.3	360	10	AF029237	AF029237 Mus muscu
41	84	19.3	639	6	107388	107388 Sequence 3
42	84	19.3	645	10	AB048528	AB048528 Mus muscu
43	83	19.1	300	10	AF137626	AF137626 Mus muscu
44	83	19.1	306	10	MUSIGKAFT	M64168 Mus musculu
45	83	19.1	436	10	MNU012556	AF012556 Mus musculu

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Copyright (c) 1993 - 2000 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: February 20, 2002, 20:40:31 ; Search time 1476.91 Seconds
(without alignments)
4858.978 Million cell updates/sec

RESULT 1

AF124721	AF124721	381 bp	mRNA	ROD	22-MAY-2001
LOCUS	Mus musculus	immunoglobulin light chain	mRNA, partial cds.		
DEFINITION					
ACCESSION	AF124721				
VERSION	AF124721.1	GI:14164546			
KEYWORDS					
SOURCE	house mouse.				
ORGANISM	Mus musculus				
Bukartha, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE 1 (bases 1 to 381)					
AUTHORS Tripathi, P.K., Oin, H., Bhattacharyya-Chatterjee, M., Ceriani, R.L., Foon, K.A. and Chatterjee, S.K.					
TITLE Construction and characterization of a chimeric fusion protein consisting of an anti-idiotypic antibody mimicking a breast cancer-associated antigen and the cytokine GM-CSF					
JOURNAL Hybrioma 18 (2), 193-202 (1999)					
MEDLINE 9936687					
PUBMED 10380019					

REFERENCE	2 (bases 1 to 381) and tripathi P.K.	JOURNAL	Mol. Immunol. 37 (15), 901-913 (2000)
AUTHORS	Chatterjee, S.K.	MEDLINE	21179651
TITLE	Direct Submission	PUBMED	11282394
JOURNAL	Submitted (29-JAN-1999) Internal Medicine, University of Kentucky, 800 Rose Street, Lexington, KY 40536, USA	REFERENCE	2 (bases 1 to 321)
FEATURES	Location/Qualifiers	AUTHORS	Mertens, N.M. and Cunningham, M.W.
Source	I. .381	TITLE	Direct Submission
CDS	/organism="Mus musculus"	JOURNAL	Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma University Health Sciences Center, 940 St. Young Blvd, Oklahoma City, OK 73190, USA
	/strain="BALB/c"	FEATURES	Location/Qualifiers
	/db_xref="taxon:10090"	SOURCE	/organism="Mus musculus"
	1. .>381		/strain="BALB/c"
	/note="anti-idiotypic antibody 1D10; mimics a breast cancer-associated antigen, human fat globule (HMGF)"		/db_xref="taxon:10090"
	/codon_start=1		/note="mAb 49.8.9"
	/product="immunoglobulin light chain"	CDS	<1. .>321
	/protein_id="AAK55120.1"		/note="V-J segments"
	/db_xref="GI:4164547"		/codon_start=1
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BASE COUNT	90 a 93 c 89 g 109 t		/db_xref="GI:5690305"
ORIGIN			/translation="DIQWTOSPSSLSASLGERVSLTCHASQDQGSSLNLQOBPDGTI
			KRLTATSSLSDSGVPKRFSGSSRSGLSDYSLTISSESDFVDYCYLQYASSPYTFGGT
Query Match	86.7%; Score 37; DB 10; Length 381;	BASE COUNT	84 a 77 c 75 g 85 t
Best Local Similarity	100.0%; Pred. No. 3.9e-218; Mismatches 0; Indels 0; Gaps 0; Matches 377; Conservative 0;	Query Match	26.9%; Score 117; DB 10; Length 321;
Db	5 GGGCCCTGCGCAGATCTTGTTCTGGTCAGCTCTGCTCTGGTTCAGGTACAGATGACA 64	Best Local Similarity	99.1%; Pred. No. 1.2e-59; Mismatches 2; Indels 0; Gaps 0; Matches 217; Conservative 0;
Qy	65 TCCAGATGACCCAGCTCCATCCTCTTATCTGCCCTCTGGACAAAGCTCAGTC 124	Db	103 TGGCTTCAGCAGAACCAAGATGGAACTATTAACCSCTGTATCTGCCCATCTA 162
Db	65 TCCAGATGACCCAGCTCCATCCTCTTATCTGCCCTCTGGACAAAGCTCAGTC 124	Qy	163 TGGCTTCAGCAGAACCAAGATGGAACTATTAACCSCTGTATCTGCCCATCTA 162
Qy	125 CTGTGCGGGCAGTCAGGACTGGTATTACTTACATTCAGTCAGCAGAACCAAGATG 184	Db	125 CTGTGCGGGCAGTCAGGACTGGTATTACTTACATTCAGTCAGCAGAACCAAGATG 184
Db	125 CTGTGCGGGCAGTCAGGACTGGTATTACTTACATTCAGTCAGCAGAACCAAGATG 184	Qy	223 GGTCTCGGGTCCCAAAGGTCAGTGGAGTAGTCGGTCAGATATTCTCACC 282
Qy	185 GAACTTAAAGGCCGATCACGCCACATCCAGTGTAGGTTAGGTTCTGGTCCCACAAGT 244	Db	163 GATTCTGGTGCCTCAAAGGTTCACTGTCAGTGGCAGTAGTGTCTGGTCAGATTA 222
Db	185 GAACTTAAAGGCCGATCACGCCACATCCAGTGTAGGTTAGGTTCTGGTCCCACAAGT 244	Qy	283 ATCAGCAGCTTGAGTCTGAGATTTGACCTTATACGTCACAAATGCTAGTC 342
Qy	245 TCACTGGCAGTAGGCTGGTCAGATTATCTCACCACAGCAGCCTGAGTCGAAG 304	Db	223 ATCAGCAGCCCTGAGTCTGAGATTTGACCTTATACGTCACAAATGCTAGTC 282
Db	245 TCACTGGCAGTAGGCTGGTCAGATTATCTCACCACAGCAGCCTGAGTCGAAG 304	Qy	343 CGTACAGCTGGAGGGGACCAAGCAGTCGAATAAA 381
Qy	305 ATTCTGCTAGCTTACTGCTACATAIGCTAGTCTCCGTACACGTTGGAGGGGG 364	Db	283 CGTACAGCTGGAGGGGACCAAGCAGTCGAATAAA 321
Db	305 ATTCTGCTAGCTTACTGCTACATAIGCTAGTCTCCGTACACGTTGGAGGGGG 364	RESULT	3
Qy	365 CCAAGCTGGAAATAAA 381	MUSIGLFA	MUSIGLFA
Db	365 CCAAGCTGGAAATAAA 381	LOCUS	303 bp mRNA
RESULT	2	DEFINITION	Mouse Ig kappa-chain mRNA V region, partial cds, from hybridoma H220-23.
AF163749	AF163749 321 bp mRNA	ACCESSION	M56246
LOCUS	Mus musculus mab 49.8.9 immunoglobulin light chain variable region	VERSTON	GT:197631
DEFINITION	mRNA, partial cds.	KEYWORDS	V-region; immunoglobulin kappa-chain; processed gene.
ACCESSION	AF163749	SOURCE	Mouse (strain BALB/c), cDNA to mRNA, from hybridoma H220-23.
VERSION	AF163749.1	ORGANISM	Mus musculus
KEYWORDS	house mouse.		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
SOURCE	mus musculus		(bases 1 to 303)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	REFERENCE	1 (bases 1 to 321)
		AUTHORS	Kavaler, J., Caton, A.J., Staudt, L.M., Schwartz, D. and Gerhard W.
		TITLE	Set of closely related antibodies dominates the primary antibody response to the antigenic site CB of the A/PR/8/34 influenza virus hemagglutinin. J. Immunol. 145, 2312-2321 (1990)
REFERENCE	1 (bases 1 to 321)	JOURNAL	90375932
AUTHORS	Mertens, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.	COMMENT	Draft entry and computer-readable sequence for [J. Immunol. (1990) In Press] kindly submitted by J. Kavaler, 06-JUL-1990.
TITLE	Molecular analysis of cross-reactive anti-myosin/anti-streptococcal mouse monoclonal antibodies	FEATURES	Location/Qualifiers

source
 /organism="Mus musculus"
 /strain="BALB/c"
 /sub_species="domesticus"
 /db_xref="taxon:10090"
 /tissue_type="hybridoma"
 /map="chromosome 6"
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 1..303
 /gene="IgM"
 CDS
 <1..>303
 /gene="IgM"
 /codon_start=1
 /product="immunoglobulin kappa-chain VK-1"
 /protein_id="AA39105.1"
 /db_xref="GI:197632"
 /translation="MTSPSSISLGERVLSTCRASQDIGSSNLWQERPDGTIKRL"
 /translatioin="MTSPSSISLGERVLSTCRASQDIGSSNLWQERPDGTIKRL"
 BASE COUNT
 78 a 71 c 70 g 83 t 1 others
 ORIGIN
 BASE COUNT
 74 a 72 c 71 g 84 t 1 others
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 Query Match 24.8%; Score 108; DB 10; Length 303;
 Best local similarity 99.0%; Pred. No. 3.8e-54;
 Matches 208; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 163 TGGCTTCAGCAGAACCGATGACTTAAACGCCATGATGTTACGCCACATCCACTTA 222
 Db 85 TGGCTTCAGCAGAACCGATGACTTAAACGCCATGATGTTACGCCACATCCAGTTA 144
 QY 223 GGTCTGGTCCCCAAAGGTCAGTOGCCAGTAGGTCTGGTCAGATTATCTCTACC 282
 Db 145 GATTCCTGGTCCAAAGGTCAGTOGCCAGTAGGTCTGGTCAGATTATCTCTACC 204
 QY 283 ATCAGCAGCCTGAGTCAGAAGGTTGAGCTTATCTGCTACATAATGCTAGTCT 342
 Db 205 ATCAGCAGCCTGAGTCAGAAGGTTGAGCTTATCTGCTACATAATGCTAGTCT 264
 QY 343 CCTPACAGTTGGAGGGGGCCAACGTG 372
 Db 265 CGGTACAGTTGGAGGGGGCCAACGTG 294
 RESULT 4
 MMU5588
 LOCUS MMU5588 302 bp mRNA ROD 05-MAR-1997
 DEFINITION MUS musculus anti-DNA immunoglobulin light chain IgG, antibody
 ACCESSION U55588
 VERSION 055588.1 GI:1870291
 KEYWORDS house mouse.
 SOURCE
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 273)
 AUTHORS Roark,J.H., Kunz,C.L., Nguyen,K.A., Mandik,L., Cattermole,M. and
 Erikson,J.
 TITLE B cell selection and allelic exclusion of an anti-DNA Ig transgene
 JOURNAL in MRL-1pr/lpr mice
 J. Immunol. 154 (9), 4444-4455 (1995)
 MEDLINE 95238842
 REFERENCE 2 (bases 1 to 273)
 AUTHORS Roark,J.H.
 TITLE Direct Submission
 JOURNAL Submitted (15-FEB-1995) Jessica H. Roark, Wistar Institute, 3601
 Spruce St., Philadelphia, PA 19104, USA
 FEATURES Source
 /organism="Mus musculus"
 /strain="MRL-1pr/lpr"
 /db_xref="taxon:10090"
 /clone="MRL3-7"
 /cell-type="splenic B cell hybridoma"
 /tissue_type="spleen"
 /dev_stage="adult"
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 /codon_start=3
 /product="immunoglobulin kappa chain variable and joining regions"
 /cell_line="363s 62"
 /cell_type="hybridoma"
 /db_xref="GI:699557"
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 /strain="(NZB x NZW) F1"
 /db_xref="taxon:10090"
 /cell_line="363s 62"
 /cell_type="hybridoma"
 /note="mouse number 363"
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 /V-region
 CDS
 <1..>302
 /codon_start=1
 /product="anti-DNA immunoglobulin light chain IgG"
 /protein_id="AAB8706.1"
 /db_xref="GI:1870292"
 /translation="MTSPSSISLGERVLSTCRASQDIGSSNLWQERPDGTIKRL"
 /translatioin="MTSPSSISLGERVLSTCRASQDIGSSNLWQERPDGTIKRL"
 /protein_id="AA39105.1"
 /db_xref="GI:699557"

Matches	150;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	163	TGGCTTCAGCAGGACCAGATGGAACTTAAACGCCGATCTACGCCACATCCAGTTA	222	Locus	MMU29617	285 bp	mRNA	ROD	08-DEC-1995
DEFINITION	Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J region, hybridoma 52-46A, partial cds.								
Db	103	TGGCTTCAGCAGGACCAGATGGAACTTAAACGCCGATCTACGCCACATCCAGTTA	162	DEFINITION	U29617				
VERSION	U29617.1	GT:896102							
KEYWORDS									
SOURCE	house mouse.								
ORGANISM	Mus musculus								
DEFINITION	Mus musculus clone 263.08 nonfunctional immunoglobulin kappa light chain variable region gene, partial sequence.	ROD	20-JUN-1999	REFERENCE	Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.				
ACCESSION	AF144956			AUTHORS	Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.				
VERSION	AF144956.1	GI:5106651		JOURNAL	J. Immunol. 155 (6), 3223-3233 (1995)				
KEYWORDS	house mouse.			MEDLINE	95u03997				
ORGANISM	Mus musculus			REFERENCE	2 (bases 1 to 285)				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				AUTHORS	Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.Z.				
REFERENCE	1 (bases 1 to 285)			JOURNAL	Princeton University, Princeton, NJ 08544, USA				
AUTHORS	Benedict,C.L. and Kearney,J.F.			FEATURES	Direct Submission				
TITLE	Increased junctional diversity in fetal B cells results in a loss of protective anti-phosphorylcholine antibodies in adult mice			SOURCE	Submitted (21-JUN-1995) Saleh M. Ibrahim, Molecular Biology, Princeton University, Princeton, NJ 08544, USA				
JOURNAL	Immunity 10 (5), 607-617 (1999)			FEATURES	Location/Qualifiers				
MEDLINE	99294326			SOURCE	1. .285				
REFERENCE	2 (bases 1 to 283)			FEATURES	/organism="MUS musculus"				
AUTHORS	Benedict,C.L. and Kearney,J.F.			SOURCE	/strain="BALB/C"				
TITLE	Direct Submission			FEATURES	/isolate="Hybridoma 52-46A"				
JOURNAL	Submitted (22-APR-1999) Department of Microbiology, University of Alabama at Birmingham, 378 Wallace Tumor Institute, Birmingham, AL 35294, USA			SOURCE	/db_xref="taxon:10090"				
FEATURES				FEATURES	/chromosome="6"				
SOURCE	1. .283			SOURCE	<1. .>285				
/organism="MUS musculus"				FEATURES	/note="V-J region"				
/db_xref="taxon:10090"				SOURCE	/codon_start1				
/clone="2653.08"				SOURCE	/product="Ig kappa chain"				
/tissue_type="liver"				SOURCE	/protein_id="PAA83103.1"				
/dev_stage="day 16 embryo"				SOURCE	/db_xref="GI:896103"				
/rearranged				FEATURES	/translation="DQWIQSPSSLASIGERVSILCRASODIGSSLNLWQOPPDGTI				
misc-f-feature	<1. .>203			SOURCE	KRLIYATSSLDGVPKRFSGRSRSDSYLSLTISSEDEPVYCLQYASSP"				
BASE COUNT	69 a			SOURCE					
ORIGIN	68 c			SOURCE					
Query Match	23.0%			SOURCE					
Best Local Similarity	99.3%			SOURCE					
Matches	150;	Conservative	0;	SOURCE					
Matches	150;	Conservative	0;	SOURCE					
Indels	0;	Mismatches	0;	SOURCE					
Gaps	0;			SOURCE					
RESULT	11			SOURCE					
103643				SOURCE					
LOCUS	I03643	324 bp ss-DNA		SOURCE					
DEFINITION	Sequence 4 from Patent US 4642334.			SOURCE					
ACCESSION	I03643			SOURCE					
VERSION	I03643.1	GI:268618		SOURCE					
KEYWORDS				SOURCE					
SOURCE	Unknown.			SOURCE					
ORGANISM	Unclassified.			SOURCE					
REFERENCE	1 (bases 1 to 324)			SOURCE					
AUTHORS	Moore,K.W. and Zafarani,A.			SOURCE					
TITLE	Hybrid DNA prepared binding composition			SOURCE					
JOURNAL	Patent: US 4642334-A 4 10-FEB-1987;			SOURCE					
DNAX Research Institute of Molecular and Cellular Biology, Inc.:				SOURCE					
Palo Alto, CA				SOURCE					
FEATURES	Location/Qualifiers			SOURCE					
RESULT	10			SOURCE					
MMU29617				SOURCE					
DEFINITION				SOURCE					
ACCESSION				SOURCE					
VERSION				SOURCE					
KEYWORDS				SOURCE					
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VERSION				SOURCE					
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SOURCE				SOURCE					
ORGANISM				SOURCE					
DEFINITION									

source	1. .324 /organism="unknown"			
BASE COUNT	82 a 80 c 75 g 87 t			
ORIGIN				
Query Match	23.0%; Score 100; DB 6; Length 324;			
Best Local Similarity	99.3%; Pred. No. 2. 9e-49;			
Matches	150; Conservative 0; Mismatches 0; Gaps 0;			
LOCUS	103 TGCCTTCAGCAGAACAGATGAACTTAAACGCCGTATCCAGTTA 162			
DEFINITION	TGGCTTCAGCAGAACAGATGAACTTAAACGCCGTATCCAGTTA 222			
ACCESSION	QY 163 TGGCTTCAGCAGAACAGATGAACTTAAACGCCGTATCCAGTTA 162			
VERSION	1			
KEYWORDS	Anti-DNA antibodies of normal mice immunized with poly(dc) are structurally similar to natural autoantibodies			
SOURCE	Unpublished			
ORGANISM	(bases 1 to 381)			
REFERENCE	Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
AUTHORS	1 (bases 1 to 381) O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.			
TITLE	Anti-DNA antibodies of normal mice immunized with poly(dc) are structurally similar to natural autoantibodies			
JOURNAL	O' Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.			
FEATURES	JOURNAL			
SOURCE	Submitted (02-FEB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA			
ORGANISM	Location/Qualifiers			
REFERENCE	2 (bases 1 to 381)			
AUTHORS	O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.			
JOURNAL	Direct Submission			
FEATURES	JOURNAL			
SOURCE	Submitted (02-FEB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA			
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REFERENCE	Direct Submission
AUTHORS	Submitted (06-FEB-1997) Biological Sciences, University of Nebraska, 325 Menter Hall, Lincoln, NE 68588-0118, USA
TITLE	Location/Qualifiers
JOURNAL	Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
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Qy	223 GGTTCTGGCTCCCCAAAGGTCACTGGCAGTAGTCGGTCAGATTCTCTCACC 282
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Qy	265 GATTCCTGGCTCCCCAAAGGTCACTGGCAGTAGTCGGTCAGATTCTCTCACC 324
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LOCUS	443 bp mRNA
DEFINITION	ROD 02-MAY-1997
ACCESSION	Mus musculus anti-DNA antibody light chain variable region mRNA, partial cds.
VERSION	U88675.1 GI:2052416
KEYWORDS	house mouse.
SOURCE	Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 443)
REFERENCE	Westhoff, C.M., Wyllie, D.E., Rathol, S., Whittier, A., McHugh, J. and Shultz, L.D.
AUTHORS	Viable notheaden anti-DNA antibody
JOURNAL	unpublished
REFERENCE	(bases 1 to 443)
AUTHORS	Westhoff, C.M., Wyllie, D.E., Rathol, S., Whittier, A., McHugh, J. and

Thu Feb 21 13:44:38 2002

us-08-836-455-1.oli.rge

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2002, 04:28:51 ; Search time 203.01 seconds
(without alignments)
1946.835 Million cell updates/sec

Title: US-08-836-455-3

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

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Minimum DB seq length: 0

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Pred. No.: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	461	100.0	461	20 AAV83773
3	76	16.5	17	AAV31333
4	76	16.5	458	20 AXA71366
5	76	16.5	458	20 AXA89553
6	76	16.5	458	20 AXA60630
7	67	14.5	861	16 AAQ81500
8	67	14.5	861	18 ACT45347
9	60	13.0	765	22 AAC86590
10	60	13.0	765	22 AAC86591
11	60	13.0	1239	22 AAC86563

ALIGNMENTS

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AC	
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XX	Murine monoclonal anti-idiotype antibody 11D10 VH cDNA.
DE	
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KW	
XX	Mus musculus.
OS	
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XX	PN W09722659-A2.
XX	PD 26-JUN-1997.
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PR	13-DEC-1996; 96US-0575762.
PR	20-DEC-1995; 95US-0575762.
PR	26-JAN-1996; 96US-0591965.
PA	(KENT) UNIV KENTUCKY.
PI	Chatterjee M, Chatterjee SK, Foon KA;

Anti-CD20 single chain antibody encoding a CD45 isoform for Ig heavy chain. Anti-CA125 bifunctional antibody. Anti-HCV Ser/Thr protein. Mouse antibody 2H7. Heavy chain variable. Mouse 2H7 antibody. Mouse 2H7 anti-idiotypic antibody. Alpha-4 integrin monoclonal antibody. Mouse anti-idiotype antibody. H-chain V-region of antibody. Heavy chain of antigen. Sequence encoding murine anti-BGH mRNA. Anti-beta1 monoclonal antibody. Combined cDNA library mRNA encoding gamma 3B1 single chain antibody. Chimeric gene construct. Plasmid p10169 encoding DNA encoding anti-mouse anti-idiotype DNA. Mouse anti-idiotype DNA encoding anti-mouse anti-idiotype Murine coding sequence.

QY 301 CAGATCAGCAGGCTGACATCTGAGACTGTGGCTTATTTCGTGCAAGAGGAACGG 360
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 ||||| anti-GD2 in a sample or measure the level of cellular anti-1A7 or
 ||||| anti-GD2 activity.

CC The cDNA can be used in expression systems for 1A7 prodn., and in
 CC the prep. of probes and primers to respect assay for 1A7
 CC cDNA, and amplify desired polynucleotides for use in gene therapy.

QY 361 GGGGGTGCTTGACTACTGGGCTAAGGAACCTCAGCACCGCTCTCACCAAAACG 420
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 ||||| ggggtgctgtactgtgggtcaaggaaacctcgtaaccgtctctccatggccaaacg 420

QY 421 AAGCCCCACCGCTATCCATGGTCCCTGGAGCTGGG 461
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 ||||| 421 aaccccacccggcttarccacggcctggtaactgg 461

Db Query Match
 RESULT 3 Best local Similarity 16.5%; Score 76; DB 17; Length 458;
 ID AAT3133 standard; CDNA; 458 BP.
 XX Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC AAT3133;
 XX DT 26-FEB-1997 (first entry)

XX Anti-idiotype monoclonal antibody 1A7 variable heavy chain, cDNA.
 DE Murine; mouse; anti-idiotype; monoclonal antibody; Mab; 1A7;
 KW variable heavy chain; ganglioside 2; GD2; neuroblastoma;
 KW glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;
 KW malignant melanoma; soft tissue sarcoma; small cell carcinoma;
 KW vaccine; treatment; palliate; detection; diagnosis;
 KW recombinant production; purification; probe; primer; assay;
 KW amplification; gene therapy; ss.
 XX OS Mus musculus.

FH Key Location/Qualifiers
 FT mat_peptide 1..456
 FT /*tag= a
 FT //transl_except= pos:373..375, aa:Trp
 XX PN W09622373-A2.
 XX PD 25-JUL-1996.
 XX PF 17-JAN-1996; 96W0-US00882.
 XX PR 16-JAN-1996; 96US-032676.
 XX PR 17-JAN-1995; 95US-037266.
 PA (KENT) UNIV KENTUCKY.
 XX PI Chatterjee M, Chatterjee SK, Foon KA;
 DR WPI; 1996-355430/35.
 DR P-PSDB; AAW0200.
 XX Monoclonal antibody 1A7 and related polynucleotide(s) and
 PT polypeptide(s) - useful to treat or palliate a GD2-associated
 PT disease, e.g. melanoma and glioma
 XX Claim 11; fig 2; 141pp; English.

PS The present sequence encodes the murine anti-idiotype monoclonal
 CC antibody (Mab) 1A7 variable heavy chain. Mab 1A7 was raised against
 CC the anti-ganglioside 2 (GD2) MAb 14G2a, which binds an unique
 CC epitope of GD2. As the glycosphingolipid GD2 is expressed at high
 CC density by human neuroectodermal tumours, e.g. malignant melanoma,
 CC neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma
 CC of the lung, Mab 1A7, or its cDNA can be used in a vaccine to treat
 CC or palliate such diseases. They can also be used to reduce the
 CC risk of recurrence of a clinically detectable tumour, and detect an
 CC anti-GD2 Ab bound to a tumour cell.
 CC Mab 1A7 overcomes immune tolerance and induces an immune response
 CC against GD2, which comprises anti-GD2 Ab (humoral response) and

CC GD2-specific cells (cellular response). It can be used to purify
 CC anti-1A7 (Ab3), anti-GD2 (Ab1) or 14G2a (Ab1), detect anti-1A7 or
 CC anti-GD2 in a sample or measure the level of cellular anti-1A7 or
 CC anti-GD2 activity.

CC The cDNA can be used in expression systems for 1A7 prodn., and in
 CC the prep. of probes and primers to respect assay for 1A7
 CC cDNA, and amplify desired polynucleotides for use in gene therapy.

CC Sequence 458 BP; 106 A; 131 C; 114 G; 107 T; 0 other;

QY 366 TGCCTGGACTACTGGGCTAAGGAACCTCAGTGACCCCTCCAGGCAAACGACCC 425
 ID AAT31366 standard; CDNA; 458 BP.
 XX Matches 363 tgcttgactactggggtaaaggaaacctcgacccttcagccaaacgacc 422
 AC AAT31366;
 XX DT 07-FEB-2000 (first entry)

XX DE Mab 1A7 heavy chain variable region encoding cDNA.
 XX KW Monoclonal antibody; Mab; 1A7; GD2; immune response; melanoma;
 KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
 KW tumor-associated antigen; ss.
 OS Synthetic.
 OS Mus sp.
 XX PN US5977316-A.
 XX PD 02-NOV-1999.
 XX PF 16-JAN-1996; 96US-0591196.
 XX PR 17-JAN-1995; 95US-032676.
 XX PA (KENT) UNIV KENTUCKY.
 XX PI Foon KA, Chatterjee SK, Chatterjee M;
 DR WPI; 1999-619711/53.
 DR P-PSDB; AAY49310.
 XX Monoclonal antibody 1A7 which elicits an anti-GD2 immunological
 PT response, useful for the development of products for the detection and
 PT treatment of cancers -
 XX PS Disclosure; fig 2; 74pp; English.

XX The invention provides a monoclonal antibody (Mab) designated 1A7, which
 CC elicits an anti-GD2 (tumor-associated antigen) immunological response in
 CC humans. Mab 1A7 has defined light and heavy chain variable region
 CC sequences. The Mab 1A7 and polypeptides can be used for eliciting an
 CC anti-GD2 immune response. The polypeptides can also be used for detecting
 CC or purifying anti-GD2 antibody. The products can be used for treating GD2
 CC -associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue
 CC carcinoma, and small cell carcinoma. They can be used for palliating the
 CC disease or for reducing the risk of recurrence. The present sequence
 CC represents the cDNA encoding the heavy chain variable region of Mab 1A7.

SQ Sequence 458 BP; 106 A; 131 C; 114 G; 107 T; 0 other;

Query Match 16.5%; score 76; DB 20; Length 458;
Best Local Similarity 100.0%; Pred. No. 9.7e-26;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 366 TCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCCTCACCCAAACGACACC 425
Db 363 tgctctgactgactgggtcaaggacacctcagtcacgatccatcgccaaacgacacc 422

Qy 426 CCCACCCGTCATCCA 441
Db 423 cccacccgtctatcca 438

RESULT 5

AAX89553

ID AAX89553 standard; cDNA; 458 BP.

XX AC

XX AAX89553;

DT 06-OCT-1999 (first entry)

XX DE Heavy chain variable region of Mab 1A7.

XX KW heavy chain variable region; antibody 1A7; T cell response; melanoma;

KW ganglioside GD2; CDR; complementarity determining region; carcinoma; ss.

XX OS mus musculus.

XX Key Location/Qualifiers

PH CDS

XX FT 1..456 /*tag= a

FT /*product= "VH chain Mab 1A7
/note= "No stop codon given"

FT 1..57 /*tag= b

FT 58..456 /*tag= c

XX US5935821-A.

XX PD 10-AUG-1999.

XX PR 21-NOV-1996; 96US-0752844.

XX PR 21-NOV-1996; 96US-0372676.

PR 17-JAN-1995; 95US-0372676.

PR 16-JAN-1995; 96US-0591196.

XX PA (KENT) UNIV KENTUCKY.

XX PI Chatterjee M, Foon KA;

XX DR WPI: 1999-34740729.

XX DR P-PSDB; AAV21546.

XX PT Treatment of psoriasis

XX PS Disclosure; Fig 3; 48pp; English.

DR WPI: 1999-457600/38.

DR P-PSDB; AAY28469.

XX Anti-GD2 immunological peptides useful for the treatment of tumours especially melanomas and small cell carcinomas

XX The sequence is the variable heavy chain region of monoclonal anti-idiotypic antibody 1A7. The polypeptide encoded by this sequence has three CDRs (complementarity determining regions). When administered to an individual the 1A7 antibody induces an immune response against ganglioside GD2. The light chain variable region of the 1A7 antibody (AAY28469) is also capable of eliciting an anti GD2 response in mammals.

CC Both the heavy and light chain variable regions of the 1A7 antibody produce anti-GD2 T cell and antibody responses. The peptides and antibodies may be useful for the modulation of ganglioside GD2, and particularly for the treatment of GD2-associated tumours (e.g. melanoma,

CC neuroblastoma, glioma, soft tissue sarcoma, and small cell carcinoma (including small cell lung cancer).

CC sequence 458 BP; 106 A; 131 C; 114 G; 107 T; 0 other;

Query Match 16.5%; score 76; DB 20; Length 458;
Best Local Similarity 100.0%; Pred. No. 9.7e-26;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 366 TCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCCTCACCCAAACGACACC 425
Db 363 tgctctgactgactgggtcaaggacacctcagtcacgatccatcgccaaacgacacc 422

Qy 426 CCCACCCGTCATCCA 441
Db 423 cccacccgtctatcca 438

RESULT 6

AAX60630

ID AAX60630 standard; cDNA; 458 BP.

XX AC

XX AAX60630;

DT 03-AUG-1999 (first entry)

XX DE Monoclonal antibody 1A7 heavy chain variable region encoding cDNA.

XX KW Psoriasis; immunological response; anti-idiotype antibody; glutamate; monoclonal antibody; 1A7; ss.

XX OS Unidentified.

XX PN WO925380-A2.

XX PD 27-MAY-1999.

XX PR 17-NOV-1998; 98WO-US24607.

XX PR 16-NOV-1998; 98US-0192838.

XX PR 17-NOV-1997; 97US-0065774.

XX PA (KENT) UNIV KENTUCKY RES FOUND.

XX PI Chatterjee M, Foon KA;

XX DR WPI: 1999-34740729.

XX DR P-PSDB; AAV21546.

XX PT Treatment of psoriasis

XX PS Disclosure; Fig 3; 48pp; English.

DR WPI: 1999-457600/38.

DR P-PSDB; AAY28469.

XX Anti-GD2 immunological peptides useful for the treatment of tumours especially melanomas and small cell carcinomas

XX The sequence is the variable heavy chain region of monoclonal anti-idiotypic antibody 1A7. The polypeptide encoded by this sequence has three CDRs (complementarity determining regions). When administered to an individual the 1A7 antibody induces an immune response against ganglioside GD2. The light chain variable region of the 1A7 antibody (AAY28469) is also capable of eliciting an anti GD2 response in mammals.

CC Both the heavy and light chain variable regions of the 1A7 antibody produce anti-GD2 T cell and antibody responses. The peptides and antibodies may be useful for the modulation of ganglioside GD2, and particularly for the treatment of GD2-associated tumours (e.g. melanoma,

RESULT	7		DT	08-AUG-1997 (first entry)
AAQ81500		GGGTTAGGACCTTGCTTCAACCGTCCTCAGCCAAACACACC	XX	
ID	AAQ81500	GGGTTAGGACCTTGCTTCAACCGTCCTCAGCCAAACACACC	DE	Single chain SFV anti-rev antibody encoding cDNA.
Db	363	tgcctcgactactgggtcaaggaaacctcagtcacccgtctccat	XX	
OY	426	ccccatccgtatcca	KW	Gene therapy; antibody; immunisation; human immunodeficiency virus;
Db	423	cocacccgttatcca	KW	HIV; human T-cell leukaemia virus; ss.
			OS	Mus musculus.
			XX	
			PN	W09637234-A1..
			PD	28-NOV-1996.
			XX	
			PP	96WO-US07393.
			XX	
			PR	23-MAY-1995; 95US-0447610.
			XX	
			PA	(UYJE-) UNIV JEFFERSON THOMAS.
			XX	
			PT	Improved gene therapy using recombinant gene coding for an antibody
			PT	- for intracellular immunisation against pathogens recognised by the
			PT	antibody, esp. human immunodeficiency virus HIV-1
			XX	
			PS	Example 4; Page 54; 213pp; English.
			XX	
			CC	The present sequence encodes a single chain SFV anti-rev antibody
			CC	constructed using variable domains of the heavy and light chains of a
			CC	murine monoclonal antibody against (HIV-1)R rev (the parent
			CC	antibody). This is incorporated into a viral vector where
			CC	expression of the anti-rev gene causes inhibition of the rev function
			CC	and so affects replication of the other virus (HIV). Rev is one of the
			CC	essential regulatory proteins of HIV. It binds to rev responsive element
			CC	(RRE) and promotes the nuclear export, stabilisation and utilisation of
			CC	the viral mRNA's containing RRE. A novel gene therapy method has been
			CC	produced, where a recombinant (rec) gene is introduced into the cells of
			CC	a mammal. The method is improved by using a rec gene encoding an
			CC	antibody (Ab) that is selectively specific for an intracellular (IC)
			CC	antigen associated with a disease. The method is used to prevent or
			CC	halt the progress of a disease by IC immunisation. Specifically, the Ab
			CC	can be used to inhibit the replication of a virus, such as human T-cell
			CC	leukaemia virus or especially HIV-1, or of other pathogens, e.g.
			CC	bacteria, fungi. The method provides immunity before or after the
			CC	development of the disease and can be used to control the severity of
			CC	the disease.
			XX	Sequence 861 BP; 199 A; 234 C; 230 G; 198 T; 0 other;
			SQ	
		Query Match	14.5%; Score 67; DB 16; Length 861;	
		Best Local Similarity	100.0%; Pred. No. 1.3e-21;	
		Matches	67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
		Matches	67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	374	ACTACTGGGGTCAAGGAACCTCAGTCACCGCTCCAGGCCAAACGACACCCCCACCG	OY	374 ACTACTGGGGTCAAGGAACCTCAGTCACCGCTCCAGGCCAAACGACACCCCCACCG
Db	792	actactgggtcaaggaaacctcagtccaccgtctccatcagccaaaacgacaccccccacccg	Db	792 actactgggtcaaggaaacctcagtccaccgtctccatcagccaaaacgacaccccccacccg
OY	434	TCTATCC 440	OY	434 TCTATCC 440
Db	852	tctatcc 858	Db	852 tctatcc 858
			RESULT	9
			ID	AAC86590 AAC86590 standard; DNA; 765 BP.
			XX	
			AC	AAC86590;
			XX	
			DT	02-APR-2001 (first entry)
			XX	

DE DNA encoding a fusion of a single chain antibody and streptavidin.
 XX KW Streptavidin; tumour cell; cancer; adenocarcinoma;
 KW hematological malignancy; ss.
 XX OS Synthetic.
 OS Streptomyces avidinii.
 OS Unidentified.

XX WO200075333-A1.
 PN PD 14-DEC-2000.
 XX PR 05-JUN-2000; 2000WO-US15595.
 XX PR 07-JUN-1999; 99US-0137900.
 PR 03-DEC-1999; 99US-0168976.
 XX PA (NBO-R-) NEORX CORP.
 PA Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
 PI XX WPI; 2001-091213/10.

PT New vector constructs for expressing genomic streptavidin fusion
 proteins which are useful for targeting tumour cells associated with
 cancer, e.g. adenocarcinomas -
 PS Example 5; Page 95; 100pp; English.

CC The present sequence encodes a fusion of an anti-CD20 single chain
 antibody and streptavidin. The fusion protein is expressed using
 CC vectors of the invention. The specification describes vector constructs
 CC for expressing streptavidin fusion proteins. The vector comprises a
 nucleic acid encoding streptavidin or its functional variant operatively
 CC linked to a promoter, and a cloning site for insertion of a second
 nucleic acid sequence encoding a polypeptide to be fused with
 CC streptavidin, interposed between the promoter and the first nucleic
 acid sequence. Alternatively, the vector construct comprises a nucleic
 CC acid, operatively linked to a promoter, encoding a polypeptide to be
 fused with streptavidin, and a cloning site for insertion of a second
 nucleic acid encoding at least 129 amino acids of streptavidin or its
 CC fused with streptavidin, and a cloning site for insertion of a second
 nucleic acid encoding at least 129 amino acids of streptavidin or its
 CC nucleic acid encoding, at least 129 amino acids of streptavidin or its
 CC functional variant. The fusion proteins are useful for targeting tumour
 cells, particularly tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct
 CC is useful for expressing of streptavidin fusion proteins. In particular,
 CC these are useful as tools for medical diagnostics and therapeutic
 CC purposes, e.g. for detecting the presence or absence of, or treating, a
 CC target site within a mammalian host.
 XX Sequence 765 BP; 169 A; 201 C; 230 G; 165 T; 0 other;

SQ Query Match 13.0%; Score 60; DB 22; Length 765;
 Best Local Similarity 100.0%; Pred. No. 2,3e-18; Mismatches 60; Conservative 0; Indels 0; Gaps 0;
 Matches 60; Other 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTACAAATGCACTGGTAAGCAGACCTGACAGGCCCTGAATGATGGA 204
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DQ 88 accagtacaaatgcactggtaagcagacactggacaggctggaaatggatgga 147
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
 AAC86591 ID AAC86591 standard; DNA; 765 BP.
 XX AC AAC86591;
 AC AAC86591;
 DT 02-APR-2001 (first entry)
 XX DE DNA encoding a fusion of a single chain antibody and streptavidin.
 KW DNA encoding a fusion of a single chain antibody/streptavidin.
 KW Streptavidin; tumour cell; cancer; adenocarcinoma;
 KW Synthetic.

KW hematological malignancy; ss.
 XX OS Synthetic.
 OS Streptomyces avidinii.
 OS Unidentified.

XX WO200075333-A1.
 PN PD 14-DEC-2000.
 XX PR 05-JUN-2000; 2000WO-US15595.
 XX PR 07-JUN-1999; 99US-0137900.
 PR 03-DEC-1999; 99US-0168976.
 XX PA (NBO-R-) NEORX CORP.
 PI Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
 DR XX WPI; 2001-091213/10.

PT New vector constructs for expressing genomic streptavidin fusion
 proteins which are useful for targeting tumour cells associated with
 cancer, e.g. adenocarcinomas -
 PS Example 5; Page 95; 100pp; English.

CC The present sequence encodes a fusion of an anti-CD20 single chain
 antibody and streptavidin. The fusion protein is expressed using
 CC vectors of the invention. The specification describes vector constructs
 CC for expressing streptavidin fusion proteins. The vector comprises a
 nucleic acid encoding streptavidin or its functional variant operatively
 CC linked to a promoter, and a cloning site for insertion of a second
 nucleic acid sequence encoding a polypeptide to be fused with
 CC streptavidin, interposed between the promoter and the first nucleic
 acid sequence. Alternatively, the vector construct comprises a nucleic
 CC acid, operatively linked to a promoter, encoding a polypeptide to be
 fused with streptavidin, and a cloning site for insertion of a second
 nucleic acid encoding at least 129 amino acids of streptavidin or its
 CC functional variant. The fusion proteins are useful for targeting tumour
 cells, particularly tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct
 CC is useful for expressing of streptavidin fusion proteins. In particular,
 CC these are useful as tools for medical diagnostics and therapeutic
 CC purposes, e.g. for detecting the presence or absence of, or treating, a
 CC target site within a mammalian host.
 XX Sequence 765 BP; 170 A; 201 C; 231 G; 163 T; 0 other;

SQ Query Match 13.0%; Score 60; DB 22; Length 765;
 Best Local Similarity 100.0%; Pred. No. 2,3e-18; Mismatches 60; Conservative 0; Indels 0; Gaps 0;
 Matches 60; Other 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ACCAGTACAAATGCACTGGTAAGCAGACCTGACAGGCCCTGAATGATGGA 204
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 88 accagtacaaatgcactggtaagcagacactggacaggctggaaatggatgga 147
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
 AAC86563 ID AAC86563 standard; DNA; 1239 BP.
 XX AC AAC86563;
 AC AAC86563;
 DT 02-APR-2001 (first entry)
 XX DE DNA encoding a fusion of anti-CD20 single chain antibody/streptavidin.
 KW Streptavidin; tumour cell; cancer; adenocarcinoma;
 KW hematological malignancy; ss.
 XX OS Synthetic.

OS Streptomyces avidinii.
 OS Homo sapiens.
 XX WO200075333-A1.
 XX 14-DEC-2000.
 XX 05-JUN-2000; 2000WO-US15595.
 XX PR 07-JUN-1999; 99US-0137900.
 XX PR 03-DEC-1999; 99US-0168976.
 XX PA (NEOR-) NEORX CORP.
 XX PT Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
 XX DR P-PSDB; AAC30694.
 XX PR New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas -
 XX Example 2; Fig 11A; 10pp; English.
 CC The present sequence encodes a fusion of an anti-CD20 single chain antibody (B9E9) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host.
 CC Sequence 1239 BP; 270 A; 392 C; 356 G; 221 T; 0 other;
 XX SQ Query Match 13.0%; Score 60; DB 22; Length 1239;
 Best Local Similarity 100.0%; Pred. No. 2.2e-18;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; gaps 0;
 Qy 145 ACCAGTGTACAAATGCACTGGTTAACGAGCACCGACAGGCCCTGGAAATGGATTGGA 204
 Db 469 accagttaataatgcactgggtaaacggacacctggacagggcctggaaatggattgga 528
 RESULT 12
 AAC86564 AAC86564 standard; DNA; 1280 BP.
 XX AAC86564;
 XX 02-APR-2001 (first entry)
 XX DE Anti-CD20 single chain antibody/streptavidin fusion protein cassette.
 XX KW Streptavidin; tumour cell; cancer; adenocarcinoma;
 XX hematochemical malignancy; ss.
 OS Synthetech.
 OS Streptomyces avidinii.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH 3..1274
 FT /tag= a
 FT /product= "anti-CD20 scFv and streptavidin fusion"
 FT PN WO200075333-A1.
 XX PD 14-DEC-2000.
 XX PR 07-JUN-1999; 99US-0137900.
 XX PR 03-DEC-1999; 99US-0168976.
 XX PA (NEOR-) NEORX CORP.
 XX PT Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
 XX DR P-PSDB; AAC30694.
 XX PR New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas -
 XX Example 2; Fig 11C; 10pp; English.
 CC The present sequence encodes a fusion of an anti-CD20 single chain antibody (B9E9) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host.
 CC Sequence 1280 BP; 267 A; 397 C; 388 G; 228 T; 0 other;
 XX SQ Query Match 13.0%; Score 60; DB 22; Length 1280;
 Best Local Similarity 100.0%; Pred. No. 2.2e-18;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; gaps 0;
 Qy 145 ACCAGTGTACAAATGCACTGGTTAACGAGCACCGACAGGCCCTGGAAATGGATTGGA 204
 Db 96 accagttaataatgcactgggtaaacggacacctggacagggcctggaaatggattgga 155
 RESULT 13
 AAC15019 AAC15019 standard; DNA; 1925 BP.
 XX AC AAC15019;
 XX DE 21-AUG-2000 (first entry)
 DE DNA encoding a CD-20 specific chimeric receptor.
 XX KW CD20-specific receptor; CD-20 specific redirected T cell; leukemia;
 KW CD20+ malignancy; non-Hodgkin's lymphoma; myeloblastic chemotherapy;
 KW stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis; ss.

XX Synthetic.
 OS Mus sp.
 XX
 FH Location/Qualifiers
 KEY 27-1928
 CDS /*tag= a
 FT 27-APR-2000.
 XX WO20023573-A2.
 PD 20-OCT-1999; 99WO-US24484.
 XX PR 20-OCT-1998; 98US-0105014.
 PA (CITY) CITY OF HOPE.
 XX PI Raubitschek A, Jensen MC, Wu AM;
 XX DR WPI; 2000-339676/29.
 XX P-PSDB; RAY84965.
 PT Genetically engineered CD20-specific redirected T cells useful for
 PT acute or chronic leukemia, and autoimmune disease -
 XX Example 1; Page 50-53; 58pp; English.
 CC The present sequence encodes a synthetic CD20-specific chimeric
 CC receptor. The specification describes CD-20 specific redirected T cells
 CC which express and bear on the cell surface membrane a CD20-chimeric
 CC receptor comprising an intracellular signalling domain, a transmembrane
 CC domain and an extracellular domain, the extracellular domain comprising
 CC a CD20-specific receptor. The genetically engineered CD20-specific
 CC redirected T cells are useful for treating a CD20+ malignancy, such
 CC as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, in a
 CC human patient having previously undergone myeoblastic chemotherapy and
 CC stem cell rescue. The genetically engineered CD20-specific redirected
 CC T cells are also useful for abrogating an untoward B cell function, such
 CC as autoimmune disease (lupus or rheumatoid arthritis) in a patient.
 XX Sequence 1925 BP; 471 A; 554 C; 541 G; 359 T; 0 other;
 SQ Query Match 13.0%; Score 60; DB 21; Length 1925;
 Best Local Similarity 100.0%; Pred. No. 2.e-18;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 145 ACCAGTTACATATGCACTGGTAAAGCAGACACTGGACAGGCCCTGGAATGGATTGGA 204
 Db 546 acacgttacatatgcaactggtaaggcagacacactggacagggcctggaaatggattgga 605
 RESULT 14
 AAT96345 AAT96345 standard; cDNA; 360 BP.
 XX
 AC AAT96345;
 XX DT 08-APR-1998 (first entry)
 DE cDNA for Ig heavy chain variable region of anti-asparaginase MAb.
 KW Immunoglobulin; Ig; heavy chain; variable region; murine;
 KW asparaginase II; monoclonal antibody; MAb;
 KW recombinant chimeric polypeptide; ss.
 OS
 XX Mus sp.
 XX US5586579-A.
 PD 11-NOV-1997.

XX PF 23-MAY-1995; 95US-0447422.
 XX PR 22-JUN-1993; 93US-008410.
 PR 21-JUN-1988; 88US-0205748.
 PR 31-AUG-1992; 92US-093505.
 PR 23-MAY-1995; 95US-0447422.
 XX PA (HYBR-) HYBRISENS LTD.
 XX PI Ramjeesingh M, Rothstein A, Shami EY;
 XX DR WPI; 1997-558200/51.
 XX PT Self-protecting chimeric polypeptide comprising biologically active
 PT sequence and single-chain antibody sequence - has resistance to e.g.
 PT disrupting temperature, presence of proteolytic enzymes, etc.
 XX PS Example 2; Columns 27-28; 29pp; English.
 XX The present sequence is the cDNA for the immunoglobulin (Ig) heavy
 CC chain variable region of a murine anti-asparaginase II monoclonal
 CC antibody (MAb). The cDNA was used in the preparation of a novel
 CC recombinant chimeric polypeptide, comprising a 1st region
 CC comprising a biologically active domain and another domain
 CC containing an epitope, linked via a polypeptide to a 2nd region
 CC including a single chain antibody (SCA) having the light and heavy
 CC chains of an antibody variable region which specifically binds the
 CC epitope in the 1st region. The chimeric polypeptide assumes a
 CC conformation in which the SCA is bound to the epitope of the 1st
 CC region and protects its biological activity from deactivation by
 CC denaturing temperatures or pH conditions, proteolytic enzymes,
 CC oxidising agents or alcohol. The regions of the chimeric
 CC polypeptide interact to form a structure analogous to an
 CC antibody-antigen complex. A L-asparaginase-SCA fusion protein of
 CC the above type has better trypsin resistance than free
 CC L-asparaginase.
 XX SQ Sequence 360 BP; 85 A; 101 C; 95 G; 79 T; 0 other;
 SQ Query Match 12.8%; Score 59; DB 18; Length 360;
 Best Local Similarity 100.0%; Pred. No. 6.9e-18;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 371 TGGACTACTGGGTCAAGGACCCAGTCACCGTCCTCAGCCAAAGCACCCCCA 429
 Db 270 tggactactgggtcaaggaaaccttcgttccctcagccaaagacacccca 328
 RESULT 15
 AAF81910 AAF81910 standard; DNA; 420 BP.
 ID AAF81910
 XX AC AAF81910;
 XX DT 08-JUN-2001 (first entry)
 XX DE Anti-CA125 bifunctional antibody VH nucleotide sequence.
 KW Anti-CA125 bifunctional antibody; cancer; immunoglobulin; tuftsin;
 KW genetic engineering; human; *Pichia pastoris*; ds.
 KW Homo sapiens.
 OS *Pichia pastoris*.
 OS Synthetic.
 XX FH Key
 FT CDS
 FT /*tag= a
 FT /partial "Anti-CA125 bifunctional antibody VH region"
 FT /product= "Anti-CA125 bifunctional antibody VH region"
 FT /transl_except= (pos:304..306,aa:Ala)

FT /notes "no start or stop codons given"
XX
PN CN1276428-A.
XX
PD 13-DEC-2000.
XX
PF 04-JUN-1999; 98CN-0107873.
XX
PR 04-JUN-1999; 98CN-0107873.
XX
PA (MAIL-) MAILING BIO-ENG CO LTD CHANGCHUN.
XX
PT LUO D, Li H, Bai Y;
XX
DR WPI; 2001-227215/24.
DR P-PSDB; RAB74791.

XX
PT Clone and expression of anti-CA125 bifunctional genetically engineered antibody -
XX
PS Claim 7; Fig 6; 27pp; Chinese.
XX
CC The present invention relates to the cloning and expression of an anti-CA125 bifunctional genetically engineered antibody and discloses a nucleotide sequence of molecular targeting medicine for cancers. For the sequence, the gene fragments in heavy-chain and light-chain variable regions of anti-CA125 immunoglobulin are used to construct single-chain antibody. The single-chain antibody gene is directly fused with the human tutsin gene. The bifunctional genetically engineered antibody expressed by the gene is composed of 259 amino acids. The recombinant expression vector with the nucleotide sequence and Pichia pastoris containing the vector are also disclosed. The present sequence encodes the specifically claimed anti-CA125 bifunctional antibody VH region.
XX
Sequence 420 BP; 103 A; 108 C; 103 G; 106 T; 0 other;

Query Match 12.8%; Score 59; DB 22; Length 420;
Best Local Similarity 100.0%; Pred. No. 6.9e-18;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 371 TGGACTCTGGGTCAGGAACCTCAGTCACCGTCTCTCACGCCAAACGAGACCCCCA 429
Db 356 tggactactgggtcaaggaaacctcagtcacccatcagaacaaacgacccca 414

Search completed: February 21, 2002, 04:28:53
Job time: 28002 sec

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GenCore version 4.5
copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 21, 2002, 04:00:25 : Search time 2044.98 seconds

(without alignments) 2434.326 Million cell updates/sec

Title: US-08-836-455-3

Perfect score: 461

Sequence: 1 ATGGGATGCAGCTGGTCCT.....CTGGTCCCTGGAAAGCTTGG 461

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: em_estfun:*

2: em_esthum:*

3: em_estin:*

4: em_estom:*

5: em_estpl:*

6: em_estba:*

7: em_estro:*

8: em_estov:*

9: em_htc:*

10: gb_est1:*

11: gb_est2:*

12: gb_htc:*

13: gb_gss:*

14: em_gss_fun:*

15: em_gss_hum:*

16: em_gss_inv:*

17: em_gss_pln:*

18: em_gss_pro:*

19: em_gss_rnd:*

20: em_gss_vrt:*

21: em_gss_other:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	59	12.8	676	10 BE369087
2	49	10.6	639	10 BE371136
3	49	10.6	802	11 BF137216
4	49	10.6	883	11 BF151077
5	49	10.6	1012	11 BF142302
6	48	10.4	718	11 BF136279
7	48	10.4	862	11 BF143948
8	47	10.2	913	11 BF503109
9	47	10.2	1384	12 AK002875
10	43	9.3	406	11 BF016722
11	42	9.1	560	11 BF181663
12	42	9.1	604	10 BE367979

ALIGNMENTS

RESULT	ID	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	COMMENT
BE369087	1	BB369087 676 bp mRNA sequence.	BB369087	BB369087.1	EST	EST	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov
								Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL) DNA sequencing by: Incyte Genomics, Inc.
								Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov
								Plate: Llam0758 row: b column: 17 High quality sequence stop: 580. Features Source
								Location/Qualifiers 1. .676 /organism="Mus musculus" /strain="CZBCH T (fetal)" /db_xref="taxon:0090" /clone=IMAGE:359320" /clone_id="NCI CGP Lu29" /tissue_type="spontaneous tumor, metastatic to mammary."

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>
 Plate: LLNL1181 row: h column: 03
 High quality sequence stop: 719.

FEATURES

source

1.

.883

Location/Qualifiers

/lab_xref="taxon:10090"
 /strain="CZECH II (fetal)"
 /clone="IMAGE:5067314"

/clone.lib="NCI CGAP Lu29"
 /tissue_type="tumor, metastatic to mammary"

/tissue_type="spontaneous tumor, metastatic to mammary."
 Stem cell origin."

/lab_host="DH10B"

/note="Organ: lung; Vector: pcMV-SPORT6; Site_1: SallI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT

211 a

268 c

217 g

187 t

ORIGIN

RESULT

BF136279

6

Query Match 10.6%; Score 49; DB 11; Length 1012;

Best Local Similarity 100.0%; Pred. No. 1.8e-14;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gaps 0; Gaps 0;

Indels 0; Gaps 0;

Mismatches 0; Indels 0; Gaps 0;

Indels 0; Gaps 0;

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Indels 0; Gaps 0;

DEFINITION	601786493F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014430 5'
ACCESSION	BFI43948
VERSION	1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	I (bases 1 to 862)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/
JOURNAL	National Institutes of Health - Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999)
TISSUE	Procurement: Gilbert Smith, Ph.D.
CONTACT	Email: cgaps-r@mail.nih.gov
CNA	Library Preparation: Life Technologies, Inc.
DNA	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
SEQUENCING	DNA Sequencing by: Incyte Genomics, Inc.
LOCATION	Clone distribution through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
PLATE	LLAM9797 row: p column: 04
High quality sequence stop:	656.
FEATURES	Location/Qualifiers
source 913 /organism="MUS musculus" /strain="RVBN" /db_xref="taxon:10090" /clone="IMAGE:4218099" /clone_id="NCI_CGAP_Co24" /lab_host="DH10B ("R1 phage-resistant)" /note="Organ: colon; Vector: PCMV-SPORE6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
High quality sequence stop:	671.
location/Qualifiers	Location/Qualifiers
source	Location/Qualifiers
I. 862 /organism="Mus musculus" /strain="CZECH II" /db_xref="taxon:10090" /clone="IMAGE:4014430" /clone_id="NCI_CGAP_Lu30" /tissue_type="tumor, metastatic to mammary" /lab_host="DH10B" /note="Organ: lung; Vector: PCMV-SPORE6; Site_1: NotI; Site_2: SalI; transgenic model WNT1, expression driven by MMV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Investigator providing samples: Gilbert Smith, NIH"	
BASE COUNT	213 a 236 c 236 g 176 t 1 others
ORIGIN	ORIGIN
Query Match	10.4%; Score 48; DB 11; Length 862;
Best Local Similarity	100.0%; Pred No. 5.7e-14;
Matches	48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	366 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 412
Db	383 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 429
RESULT	9
LOCUS	AK002875 1384 bp mRNA
DEFINITION	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library clone:0610041A01, full insert sequence.
ACCESSION	AK002875
VERSION	AK002875.1
KEYWORDS	CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone_id:RIKEN full-length enriched mouse cDNA library clone:0610041A01.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 1384)
AUTHORS	Carninci,P. and Hayashizaki,Y.
JOURNAL	Methods in enzymology. 303, 19-44 (1999)
YEAR	1999
DEFINITION	mRNA sequencing.
ACCESSION	BF583109
VERSION	1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	2 (bases 1 to 1384)
AUTHORS	Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
YEAR	2000
DEFINITION	Genome research. 10 (10), 1617-1630 (2000)
ACCESSION	BF583109
VERSION	1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	3 (bases 1 to 1384)
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akimaya,J., Nishi,R., Hizumai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishihine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wakabayashi,M., Yoneda,Y., Ichikawa,T., Ozawa,K., Tanaka,T., Matsunaga,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
COMMENT	Email: cgaps-r@mail.nih.gov
TISSUE	Tissue Procurement: Jeffrey E. Green, M.D.
CNA	Library Preparation: Life Technologies, Inc.
DNA	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
SEQUENCING	DNA Sequencing by: Incyte Genomics, Inc.
LOCATION	Clone distribution through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
PLATE	LLAM9797 row: p column: 04
High quality sequence stop:	656.
FEATURES	Location/Qualifiers
source	Location/Qualifiers
I. 913 /organism="MUS musculus" /strain="RVBN" /db_xref="taxon:10090" /clone="IMAGE:4218099" /clone_id="NCI_CGAP_Co24" /lab_host="DH10B ("R1 phage-resistant)" /note="Organ: colon; Vector: PCMV-SPORE6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	183 a 261 c 250 g 219 t
ORIGIN	ORIGIN
Query Match	10.2%; Score 47; DB 11; Length 913;
Best Local Similarity	100.0%; Pred No. 1.9e-13;
Matches	47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	366 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 412
Db	383 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 429
RESULT	9
LOCUS	AK002875 1384 bp mRNA
DEFINITION	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library clone:0610041A01, full insert sequence.
ACCESSION	AK002875
VERSION	AK002875.1
KEYWORDS	CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone_id:RIKEN full-length enriched mouse cDNA library clone:0610041A01.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	2 (bases 1 to 1384)
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shiba,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
YEAR	2000
DEFINITION	Genome research. 10 (10), 1617-1630 (2000)
ACCESSION	BF583109
VERSION	1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	3 (bases 1 to 1384)
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akimaya,J., Nishi,R., Hizumai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishihine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wakabayashi,M., Yoneda,Y., Ichikawa,T., Ozawa,K., Tanaka,T., Matsunaga,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
COMMENT	Email: cgaps-r@mail.nih.gov
TISSUE	Tissue Procurement: Jeffrey E. Green, M.D.
CNA	Library Preparation: Life Technologies, Inc.
DNA	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
SEQUENCING	DNA Sequencing by: Incyte Genomics, Inc.
LOCATION	Clone distribution through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
PLATE	LLAM9797 row: p column: 04
High quality sequence stop:	656.
FEATURES	Location/Qualifiers
source	Location/Qualifiers
I. 913 /organism="MUS musculus" /strain="RVBN" /db_xref="taxon:10090" /clone="IMAGE:4218099" /clone_id="NCI_CGAP_Co24" /lab_host="DH10B ("R1 phage-resistant)" /note="Organ: colon; Vector: PCMV-SPORE6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	183 a 261 c 250 g 219 t
ORIGIN	ORIGIN
Query Match	10.2%; Score 47; DB 11; Length 913;
Best Local Similarity	100.0%; Pred No. 1.9e-13;
Matches	47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	366 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 412
Db	383 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 429
RESULT	9
LOCUS	AK002875 1384 bp mRNA
DEFINITION	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library clone:0610041A01, full insert sequence.
ACCESSION	AK002875
VERSION	AK002875.1
KEYWORDS	CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone_id:RIKEN full-length enriched mouse cDNA library clone:0610041A01.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	2 (bases 1 to 1384)
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shiba,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
YEAR	2000
DEFINITION	Genome research. 10 (10), 1617-1630 (2000)
ACCESSION	BF583109
VERSION	1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	3 (bases 1 to 1384)
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akimaya,J., Nishi,R., Hizumai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishihine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wakabayashi,M., Yoneda,Y., Ichikawa,T., Ozawa,K., Tanaka,T., Matsunaga,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
COMMENT	Email: cgaps-r@mail.nih.gov
TISSUE	Tissue Procurement: Jeffrey E. Green, M.D.
CNA	Library Preparation: Life Technologies, Inc.
DNA	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
SEQUENCING	DNA Sequencing by: Incyte Genomics, Inc.
LOCATION	Clone distribution through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
PLATE	LLAM9797 row: p column: 04
High quality sequence stop:	656.
FEATURES	Location/Qualifiers
source	Location/Qualifiers
I. 913 /organism="MUS musculus" /strain="RVBN" /db_xref="taxon:10090" /clone="IMAGE:4218099" /clone_id="NCI_CGAP_Co24" /lab_host="DH10B ("R1 phage-resistant)" /note="Organ: colon; Vector: PCMV-SPORE6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	183 a 261 c 250 g 219 t
ORIGIN	ORIGIN
Query Match	10.2%; Score 47; DB 11; Length 913;
Best Local Similarity	100.0%; Pred No. 1.9e-13;
Matches	47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	366 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 412
Db	383 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 429
RESULT	9
LOCUS	AK002875 1384 bp mRNA
DEFINITION	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library clone:0610041A01, full insert sequence.
ACCESSION	AK002875
VERSION	AK002875.1
KEYWORDS	CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone_id:RIKEN full-length enriched mouse cDNA library clone:0610041A01.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	2 (bases 1 to 1384)
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shiba,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
YEAR	2000
DEFINITION	Genome research. 10 (10), 1617-1630 (2000)
ACCESSION	BF583109
VERSION	1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	3 (bases 1 to 1384)
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akimaya,J., Nishi,R., Hizumai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishihine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wakabayashi,M., Yoneda,Y., Ichikawa,T., Ozawa,K., Tanaka,T., Matsunaga,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
COMMENT	Email: cgaps-r@mail.nih.gov
TISSUE	Tissue Procurement: Jeffrey E. Green, M.D.
CNA	Library Preparation: Life Technologies, Inc.
DNA	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
SEQUENCING	DNA Sequencing by: Incyte Genomics, Inc.
LOCATION	Clone distribution through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
PLATE	LLAM9797 row: p column: 04
High quality sequence stop:	656.
FEATURES	Location/Qualifiers
source	Location/Qualifiers
I. 913 /organism="MUS musculus" /strain="RVBN" /db_xref="taxon:10090" /clone="IMAGE:4218099" /clone_id="NCI_CGAP_Co24" /lab_host="DH10B ("R1 phage-resistant)" /note="Organ: colon; Vector: PCMV-SPORE6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	183 a 261 c 250 g 219 t
ORIGIN	ORIGIN
Query Match	10.2%; Score 47; DB 11; Length 913;
Best Local Similarity	100.0%; Pred No. 1.9e-13;
Matches	47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	366 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 412
Db	383 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 429
RESULT	9
LOCUS	AK002875 1384 bp mRNA
DEFINITION	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library clone:0610041A01, full insert sequence.
ACCESSION	AK002875
VERSION	AK002875.1
KEYWORDS	CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone_id:RIKEN full-length enriched mouse cDNA library clone:0610041A01.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	2 (bases 1 to 1384)
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shiba,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
YEAR	2000
DEFINITION	Genome research. 10 (10), 1617-1630 (2000)
ACCESSION	BF583109
VERSION	1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	3 (bases 1 to 1384)
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akimaya,J., Nishi,R., Hizumai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishihine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wakabayashi,M., Yoneda,Y., Ichikawa,T., Ozawa,K., Tanaka,T., Matsunaga,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
COMMENT	Email: cgaps-r@mail.nih.gov
TISSUE	Tissue Procurement: Jeffrey E. Green, M.D.
CNA	Library Preparation: Life Technologies, Inc.
DNA	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
SEQUENCING	DNA Sequencing by: Incyte Genomics, Inc.
LOCATION	Clone distribution through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
PLATE	LLAM9797 row: p column: 04
High quality sequence stop:	656.
FEATURES	Location/Qualifiers
source	Location/Qualifiers
I. 913 /organism="MUS musculus" /strain="RVBN" /db_xref="taxon:10090" /clone="IMAGE:4218099" /clone_id="NCI_CGAP_Co24" /lab_host="DH10B ("R1 phage-resistant)" /note="Organ: colon; Vector: PCMV-SPORE6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	183 a 261 c 250 g 219 t
ORIGIN	ORIGIN
Query Match	10.2%; Score 47; DB 11; Length 913;
Best Local Similarity	100.0%; Pred No. 1.9e-13;
Matches	47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	366 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 412
Db	383 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 429
RESULT	9
LOCUS	AK002875 1384 bp mRNA
DEFINITION	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library clone:0610041A01, full insert sequence.
ACCESSION	AK002875
VERSION	AK002875.1
KEYWORDS	CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone_id:RIKEN full-length enriched mouse cDNA library clone:0610041A01.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	2 (bases 1 to 1384)
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shiba,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
YEAR	2000
DEFINITION	Genome research. 10 (10), 1617-1630 (2000)
ACCESSION	BF583109
VERSION	1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	3 (bases 1 to 1384)
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akimaya,J., Nishi,R., Hizumai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishihine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wakabayashi,M., Yoneda,Y., Ichikawa,T., Ozawa,K., Tanaka,T., Matsunaga,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
COMMENT	Email: cgaps-r@mail.nih.gov
TISSUE	Tissue Procurement: Jeffrey E. Green, M.D.
CNA	Library Preparation: Life Technologies, Inc.
DNA	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
SEQUENCING	DNA Sequencing by: Incyte Genomics, Inc.
LOCATION	Clone distribution through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
PLATE	LLAM9797 row: p column: 04
High quality sequence stop:	656.
FEATURES	Location/Qualifiers
source	Location/Qualifiers
I. 913 /organism="MUS musculus" /strain="RVBN" /db_xref="taxon:10090" /clone="IMAGE:4218099" /clone_id="NCI_CGAP_Co24" /lab_host="DH10B ("R1 phage-resistant)" /note="Organ: colon; Vector: PCMV-SPORE6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	183 a 261 c 250 g 219 t
ORIGIN	ORIGIN
Query Match	10.2%; Score 47; DB 11; Length 913;
Best Local Similarity	100.0%; Pred No. 1.9e-13;
Matches	47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	366 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 412
Db	383 TGCTCTGGACTACTGGGGTCAGGAACCTAGTCACCGTCCTCTAG 429
RESULT	9
LOCUS	AK002875 1384 bp mRNA

ORGANISM										
	Mus musculus									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.										
REFERENCE	/db/xref="IMAGE:3390678"									
AUTHORS	/clone.lib="NCI_CGAP_Lu29"									
TITLE	/tissue_type="spontaneous tumor, metastatic to mammary."									
JOURNAL	/stem_cell_origin."									
COMMENT	/lab_host="DH10B"									
Contact:	Robert Straussberg, Ph.D.									
Email:	cgsbps@email.nih.gov									
Tissue Procurement:	Jeffrey E. Green, M.D.									
CDNA Library Preparation:	Life Technologies, Inc.									
CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LNU)									
DNA Sequencing by:	Incyte Genomics, Inc.									
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNU at:									
http://image.llnl.gov										
Plate: LNUA8759 row: a column: 15										
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152	a	128	c	133	g	147	t			
FEATURES										
source										
BASE COUNT										
152	a	128	c	133	g	147	t			
Query Match	9.1%	Score	42;	DB	11;	Length	560;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
FEATURES										
source										
BASE COUNT										
152	a	128	c	133	g	147	t			
Query Match	9.1%	Score	42;	DB	10;	Length	604;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
133	a	172	c	165	g	134	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
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BASE COUNT										
154	a	177	c	165	g	154	t			
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Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
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154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
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Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score	42;	DB	11;	Length	650;			
Best Local Similarity	100.0%	Pred.	No.	7.e-11;						
Matches	42;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
BASE COUNT										
154	a	177	c	165	g	154	t			
Query Match	9.1%	Score</								

Db 433 TGGACTACTGGGTCAGAACCTCAGTCACCGTCTCCAG 474

RESULT 14

DEFINITION BG963642 mRNA sequence.

ACCESSION BG963642

VERSION BG963642.1

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 666)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabps-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at:

<http://image.liln.gov>

Plate: LILN0987 row: e column: 12

High quality sequence stop: 658.

Location/Qualifiers

1..666

/organism="Mus musculus"

/strain="FVB/N"

/ab_xref="taxon:10090"

/clone="IMAGE:4883155"

/clone.lib="NCI_CGAP_Co24"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.6 kb. Constructed by Life

Technologies Note: this is a NCI_CGAP Library."

BASE COUNT 173 a 177 c 164 g 157 t

ORIGIN NIH

Query Match 9.1%; Score 42; DB 11; Length 671; Best local similarity 100.0%; Pred. No. 7.2e-11; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 371 TGGACTACTGGGTCAGAACCTCAGTCACGGTCTCTCAG 412

Db 374 TGGACTACTGGGTCAGAACCTCAGTCACCGTCTCTCAG 415

Search completed: February 21, 2002, 04:00:29
Job time: 26463 sec

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at:

<http://image.liln.gov>

Plate: LILN0309 row: d column: 22

High quality sequence stop: 669.

Location/Qualifiers

1..671

/organism="Mus musculus"

/strain="C57/B6"

/db_xref="taxon:10090"

/clone="IMAGE:4055429"

/clone.lib="NCI_CGAP_Mam5"

/tissue_type="tumor, gross tissue"

/dev_stages="7 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,

BASE COUNT 173 a 177 c 164 g 157 t

ORIGIN NIH

Query Match 9.1%; Score 42; DB 11; Length 671; Best local similarity 100.0%; Pred. No. 7.2e-11; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 371 TGGACTACTGGGTCAGAACCTCAGTCACGGTCTCTCAG 412

Db 374 TGGACTACTGGGTCAGAACCTCAGTCACCGTCTCTCAG 415

Search completed: February 21, 2002, 04:00:29
Job time: 26463 sec

RESULT 15

DEFINITION BF182141 mRNA

LOCUS 601804682F1 NCI_CGAP_Mam5 Mus musculus EST

DEFINITION mRNA sequence.

ACCESSION BF182141

VERSION BF182141.1

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 671)

NIH-MGC <http://mgc.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabps-r@mail.nih.gov

Thu Feb 21 13:44:44 2002

us-08-836-455-3.oli.rst

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2002, 04:25:14 ; Search time 1476.91 Seconds

(without alignments)
5149.400 Million cell updates/sec

Title: US-08-836-455-3

Perfect score: 461

Sequence: 1 ATGGATGAGCTGGTCTT.....CTGGTCCTGGAAAGCTTGGG 461

Scoring table: ORIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1472140 seqs, 8248589755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : GenBank*

1: qb_ba:*

2: qb_htg:*

3: qb_in:*

4: qb_on:*

5: qb_ov:*

6: qb_Pat:*

7: qb_Ph:*

8: qb_Pl:*

9: qb_pr:*

10: qb_ro:*

11: qb_sts:*

12: qb_sy:*

13: qb_un:*

14: qb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_on:*

20: em_or:*

21: em_ov:*

22: em_pat:*

23: em_Ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_vl:*

30: em_htgo_hum:*

31: em_htgo_inv:*

32: em_htgo_rod:*

33: em_htg_hum:*

34: em_htg_inv:*

35: em_htg_rod:*

36: em_htg_other:*

Result No.	Score	Query Match Length	DB ID	Description
1	407	88.3	411 10 AF124720	AF124720 Mus muscu
2	96	20.8	294 10 AF303872	AF303872 Mus muscu
3	83	18.0	735 12 SC020760	AT250760 Mus muscu
4	77	16.7	902 12 XXU49832	U49832 Synthetic s
5	76	16.5	458 6 AR083801	AR083801 Sequence
6	66	14.3	484 10 MUSICH4C11	M5977 Mus musculu
7	66	14.3	490 10 MUSIGAC1A	M24785 Mouse anti-
8	61	13.2	453 10 MN024114	U24114 Mus musculus
9	60	13.0	279 10 MMIGCVRG	Z22453 M_musculus
10	60	13.0	282 10 MMIGCVRB	Z22543 M_musculus
11	60	13.0	285 10 MMIGCVRC	Z22445 M_musculus
12	60	13.0	290 10 MMIGCVRF	Z22551 M_musculus
13	60	13.0	294 10 AF303873	AF303873 Mus muscu
14	60	13.0	302 10 MMIGCVRI	Z22457 M_musculus
15	60	13.0	303 10 MMIGCVRD	Z27338 M_musculus
16	60	13.0	305 10 MMIGCVRE	AZ057984 Synthetic
17	60	13.0	352 10 MMMD0C	AX057985 Sequence
18	60	13.0	355 10 MMMD4C	AF025449 Mus muscu
19	60	13.0	358 10 MMMD01C	AX057945 Sequence
20	60	13.0	358 10 MMMD2C	AY028960 Mus muscu
21	60	13.0	360 6 AX057947	AF277091 Synthetic
22	60	13.0	765 6 AX057984	AX057984 Sequence
23	60	13.0	765 6 AX057985	AX057985 Sequence
24	60	13.0	959 10 AF025445	AY025445 Mus muscu
25	60	13.0	1239 6 AX057945	AX057945 Sequence
26	60	13.0	1280 6 AX057947	AX057947 Sequence
27	59	12.8	361 6 I73511	I73511 Sequence 14
28	59	12.8	368 10 NMEDD4	X97335 M_musculus
29	59	12.8	381 10 S72314	S72314 anti-estradi
30	59	12.8	384 10 MUSICHVA1A	M97861 Mouse hybrid
31	59	12.8	390 10 MUSL7IGHV	M97876 Mouse hybrid
32	59	12.8	396 10 AY028960	AY028960 Peptide fra
33	59	12.8	399 10 MMUD2270	A1752270 Mus muscu
34	59	12.8	401 6 A18395	A18395 Human uPA C
35	59	12.8	414 10 AF006832	AF006832 Mus muscu
36	59	12.8	420 10 MMIG15GV	X56392 Mouse mAB-1
37	59	12.8	444 10 MUSIGHEB	M13330 Mouse Ig ga
38	59	12.8	447 6 E26040	E26040 Peptide fra
39	59	12.8	458 6 105921	A1752271 Sequence 37
40	59	12.8	458 6 108811	108811 Sequence 12
41	59	12.8	458 6 109199	109199 Sequence 38
42	59	12.8	458 6 M17953	M17953 Mouse Ig re
43	59	12.8	470 6 AR059286	AR059286 Sequence
44	59	12.8	477 6 AR080860	AR080860 Sequence
45	59	12.8	480 10 MUSIGHP	M16163 Mouse Ig ga

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1

AF124720	411 bp	mRNA	ROD	22-MAY-2001
LOCUS	MUS	musculus	immunoglobulin heavy chain mRNA	
DEFINITION				
ACCESSION	AF124720			
VERSION	AF124720.1	GI:14164544		

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 411)

REFERENCE

Tripathi,P.K., Qin,H., Bhattacharya-Chatterjee,M., Ceriani,R.L., Foon,K.A. and Chatterjee,S.K.

Construction and characterization of a chimeric fusion protein consisting of an anti-idiotypic antibody mimicking a breast cancer-associated antigen and the cytokine GM-CSF

TITLE

JOURNAL

Hybridoma 18 (2), 193-202 (1999)

PUBMED

93036687

10380019

CDS

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</organism="Mus musculus"
</db_xref="taxon:10090"
1. . 367. . 411
</note="(Gly4Ser)3 linker sequence"
412. . 735
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412. . 735
</organism="Mus musculus"
</db_xref="taxon:10090"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.4e-37;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 263 CATTGACTGCAGACATCCCTCAGCACAGCCTACATGCCAGATCAGGCCCTGACATCTG 322
Db 206 CATGACTGCAGACATCCCTCAGCACAGCCTACATGCCAGATCAGGCCCTGACATCTG 265

OY 323 AAGACTCTGGCTCTATTCTGT 345
Db 266 AAGACTCTGGCTCTATTCTGT 288

RESULT 4

XNU49832 LOCUS xnu9832 902 bp mRNA
DEFINITION Synthetic single chain Fv antibody against potato virus V coat
ACCESSION U49832
VERSION U49832.1 GI:1236090
KEYWORDS

SOURCE synthetic construct.
ORGANISM synthetic construct
ARTIFICIAL sequence.

REFERENCE 1. (bases 1 to 902)
AUTHORS Chen,Z.C., Cockburn,W., Torrance,L., Barker,H. and Whitelam,G.C.
TITLE JOURNAL
JOURNAL Unpublished
REFERENCE 2. (bases 1 to 902)
AUTHORS Chen,Z.C., Cockburn,W., Torrance,L., Barker,H. and Whitelam,G.C.
TITLE JOURNAL
JOURNAL Submitted (23-FEB-1996) Z.C. Chen, Botany, Univ. of Leicester, University Road, Leicester LE1 7RH, UK
LOCATION/QUALIFIERS
1. . 902
</source
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</db_xref="taxon:32630"
</note="PCR synthesised gene from mouse hybridoma cell line"

	/translation="GAELVKGASVYKMSCKASGYTFTSNHWYKOTPGOLENIGAI	Qy	145 ACCAGTTACATAATGCACTGGTAAGCAGACACCTGGACAGGGCTGGATGGATTGA 204
BASE COUNT	74 a 68 c 80 g 60 t	Db	67 ACCAGTTACATAATGCACTGGTAANGCAGACACCTGGACAGGGCTGGATGGATTGA 126
ORIGIN			
Query Match	13.0%; Score 60; DB 10; Length 282;		
Best Local Similarity	100.0%; Pred. No. 6.1e-24; Length 285;		
Matches	60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	67 ACCAGTTACATAATGCACTGGTAANGCAGACACCTGGACAGGGCTGGATGGATTGA 126		
RESULT 11			
MNIGGVRC	13.0%; Score 60; DB 10; Length 282;		
LCUCS	Best Local Similarity 100.0%; Pred. No. 6.1e-24; Length 282;		
DEFINITION	Mus musculus immunoglobulin gamma heavy chain (DBA/1) gene, v region.		
ACCESSION	M.musculus immunoglobulin gamma heavy chain (DBA/1) gene, v region.		
VERSION	Z22545.1 GI:407820		
KEYWORDS	heavy chain; IgG gene; immunoglobulin; variable region.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 285)		
AUTHORS	Mo,J.A., Bona,C.A. and Holmdahl,R.		
TITLE	Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen (bases 1 to 285)		
JOURNAL	Eur. J. Immunol. (1993) In press		
REFERENCE	2 (bases 1 to 285)		
AUTHORS	Mo,J.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-AUG-1993) John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden		
REFERENCE	3 (bases 1 to 285)		
AUTHORS	Mo,J.A., Bona,C.A. and Holmdahl,R.		
TITLE	Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen (bases 1 to 290)		
JOURNAL	European Journal of Immunology. 23 (10), 2503-2510 (1993)		
MEDLINE	94009207		
PUBMED	7691608		
FEATURES	Location/Qualifiers		
source	1. . 285		
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	/strain="DBA/1"		
	/db_xref="taxon:10090"		
	/chromosome="12"		
	/dev_stage="adult"		
	/tissue_type="lymph node"		
	/cell_type="B cell hybridoma"		
	/cell_line="C1CB334 hybridoma"		
V_region	1. . 290		
gene	/gene="IgG"		
CDS	1. . 290		
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	/gene="IgG"		
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BASE COUNT	77 a 69 c 83 g 61 t		
ORIGIN			
Query Match	13.0%; Score 60; DB 10; Length 290;		
Best Local Similarity	100.0%; Pred. No. 6.1e-24; Length 290;		
Matches	60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	145 ACCAGTTACATAATGCACTGGTAANGCAGACACCTGGACAGGGCTGGATGGATTGA 204		
Db	67 ACCAGTTACATAATGCACTGGTAANGCAGACACCTGGACAGGGCTGGATGGATTGA 126		
RESULT 13			
AF303873	AF303873 294 bp mRNA		
LOCUS	ROD 10-DEC-2000		

Query Match 13.0%; Score 60; DB 10; Length 285;
 Best Local Similarity 100.0%; Pred. No. 6.1e-24;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DEFINITION	Mus musculus clone J58.42 immunoglobulin heavy chain variable region mRNA, partial cds.
ACCESSION	Mo.J.A., Bona,C.A. and Holmdahl,R.
VERSION	AF303873.1 GI:11612052
KEYWORDS	Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
SOURCE	European Journal of Immunology. 23 (10), 2503-2510 (1993)
ORGANISM	house mouse.
MUS	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
REFERENCE	Unpublished
AUTHORS	Haines,B.B., Angeles,C.V., Parmelee,A.P., McLean,P.A. and Brodeur,P.H.
TITLE	Germline diversity of the expressed BALB/c Vhu558 gene family
JOURNAL	Submitted (08-SEP-2000) Pathology, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
FEATURES	Direct Submission Location/Qualifiers
source	1..294
CDS	/organism="Mus musculus" /strain="BALB/cByJ" /db_xref="taxon:10090" /chromosome="12" /clone="J58.42" /tissue_type="spleen" /note="isolated from IgM mRNA from lipopolysaccharide-stimulated cells" <1 ..>294 /note="Vhu558 family" /codon_start=1 /product="immunoglobulin heavy chain variable region" /protein_id="AAG9154.1" /db_xref="GI:11612053" /translation="QVQLQQGELVKPGASVSKMSCKASGVFTSYNNHHWKOTPGCG LEWIGAIIPGNGDTSYKRFKGATLADKSSTAYMOLSLTSEDAVYCAR"
BASE COUNT	80 a 73 c 78 g 63 t
ORIGIN	
RESULT	14
MMIGCVRI	MMIGCVRI
LOCUS	302 bp mRNA
DEFINITION	M. musculus immunoglobulin gamma heavy chain (DBA/1) gene, v region.
ACCESSION	Z25457.1 GI:407826
VERSION	225447.1 GI:407816
KEYWORDS	heavy chain; IgG gene; immunoglobulin; variable region.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 302)
AUTHORS	Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE	Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL	Eur. J. Immunol. (1993) In press
REFERENCE	2 (bases 1 to 303)
AUTHORS	Mo,J.A.
TITLE	Direct Submission
JOURNAL	Submitted (02-AUG-1993) John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE	3 (bases 1 to 303)
AUTHORS	Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE	Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL	Eur. J. Immunol. (1993) In press
REFERENCE	2 (bases 1 to 302)
AUTHORS	Mo,J.A.
TITLE	Direct Submission
JOURNAL	Submitted (02-AUG-1993) John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
FEATURES	Location/Qualifiers
source	1..303
REFERENCE	3 (bases 1 to 302)
AUTHORS	Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE	Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL	European Journal of Immunology. 23 (10), 2503-2510 (1993)
MEDLINE	94009207
PUBMED	7691608
FEATURES	Location/Qualifiers
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AUTHORS	/strain="DBA/1"
TITLE	/db_xref="taxon:10090" /chromosome="12" /dev_stage="adult" /tissue_type="lymph node" /cell_type="B cell hybridoma" /cell_line="CLICB391 hybridoma"
JOURNAL	
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JOURNAL	
FEATURES	
source	83 a 74 c 82 g 63 t
BASE COUNT	
ORIGIN	
RESULT	15
MMIGCVRD	MMIGCVRD
LOCUS	303 bp mRNA
DEFINITION	M. musculus immunoglobulin gamma heavy chain (DBA/1) gene, v region.
ACCESSION	Z25447
VERSION	225447.1 GI:407816
KEYWORDS	heavy chain; IgG gene; immunoglobulin; variable region.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 303)
AUTHORS	Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE	Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL	Eur. J. Immunol. (1993) In press
REFERENCE	2 (bases 1 to 303)
AUTHORS	Mo,J.A.
TITLE	Direct Submission
JOURNAL	Submitted (02-AUG-1993) John A Mo, Department of Medical and Physiological, Department of, Medical and Physiological Chemistry, Husargatan 3, Uppsala, 75123, Sweden
REFERENCE	3 (bases 1 to 303)
AUTHORS	Mo,J.A., Bona,C.A. and Holmdahl,R.
TITLE	Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen
JOURNAL	Euro. J. Immunol. (1993) In press
MEDLINE	94009207
PUBMED	7691608
FEATURES	Location/Qualifiers
source	1..303

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QY  145 ACCAGTACAAATGCACTGGTAAGCAGAGACCTGGACAGGCCCTGGAAATGGATGGA 204
DB  88 ACCAGTTACAATAATGCACCTGGTAAACGAGACCCUGGACAGGGCCCTGGAAATGGATGGA 147

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Search completed: February 21, 2002, 04:25:16
Job time: 2.885 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2002, 20:42:11 ; search time 203-01 Seconds
(without alignments) 1837.035 Million cell updates/sec

Title: US-08-836-455-1
Perfect score: 435
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	435	100-0	435	18 AAT85149	Murine monoclonal antibody 11D10 lig Murine anti-human Mouse derived RT3
2	435	100-0	435	20 AAV83772	Antibody 11D10 lig Murine anti-human Mouse derived RT3
3	102	23-4	387	18 AAT77851	Murine anti-human Mouse derived RT3
4	100	23-0	276	20 AAX0879	Mouse derived RT3
5	100	23-0	276	20 AAX0875	Mouse derived RT3
6	100	23-0	450	4 AAN30165	Sequence encoding Consensus DNA seq
7	93	21-4	535	19 AAV20086	DNA encoding anti-Mouse monoclonal a Human secreted exp Antibody 3G2 light
8	90	20-7	438	16 AAQ90431	
9	85	19-5	642	18 AAT85091	
10	85	19-5	651	21 AAA4344	
11	85	19-5	652	17 AAT87818	

ALIGNMENTS

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		XX	
		AC	AAT85149;
		DT	04-JAN-1998 (first entry)
		XX	
		DE	Murine monoclonal anti-idiotype antibody 11D10 VL cDNA.
		KW	Monoclonal antibody 11D10; anti-idiotype antibody; mucin; human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss.
		KW	
		OS	Mus musculus.
		XX	
		FN	Location/Qualifiers
		FT	sig_peptide 1..60
		FT	/tag= a
		FT	61..435
		FT	/*tag= b
		XX	WO9722699-A2.
		XX	
		PD	26-JUN-1997.
		XX	
		PP	19-DEC-1996; 96WO-US20757.
		XX	
		PR	13-DEC-1996; 96US-0515762.
		PR	20-DEC-1995; 95US-0515762.
		PR	26-JAN-1996; 96US-0519165.
		PA	(KENT) UNIV KENTUCKY.
		PI	Chatterjee M, Chatterjee SK, Foon KA;

Db 241 aggttcagtggcagtagctcggtgcagattatctctcacatcagacgcttgcgtct 300
 QY 301 GAGAGATTGTAATCTTACTGTCATAATGCTACGTTGGGGGG 360
 Db 301 gaagattttgtagcttactgtcataatgtatgcgttcgcacgttcggagg 360
 QY 361 GGGACCAACCTGGAAATAAACGGCTGTGTCACCAACIGTATCCATCCTCCACCA 420
 Db 361 gggaccasgctggaaataaacggctgtatgtcggaccaactgtatccatccaca 420
 QY 421 TCCAGTAACCTCGG 435
 Db 421 tccatgtgggg 435
 RESULT 3
 ATAT77851
 ID AAT77851 standard; CDNA: 387 BP.
 XX
 AC AAT77851;
 DT 03-NOV-1997 (first entry)
 XX
 DE Murine anti-human class II monoclonal antibody 44H104 VL chain cDNA.
 XX
 KW Antibody; light chain; variable region; hybridoma cell line 44H104;
 KW immune response; enhance; stimulate; vaccine; immunodiagnosis;
 KW antigen delivery; ss.
 OS MUS musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..387
 FT /tag= a
 FT note= "Encodes 44H104 light chain variable region,
 codon not given"
 FT including secretion signal; termination
 FT
 W09640941-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-CA00400.
 XX
 PR 07-JUN-1995; 95US-0483576.
 XX
 PA (CONN-) CONNAUGHT LAB LTD.
 XX
 PI Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH;
 XX
 DR WPI: 1997-07271/07.
 DR P-PSDB; AAW22537.
 XX
 PT Recombinant conjugate antibody mol', modified for delivering an
 PT antigen - elicits enhanced immune response without the use of
 PT adjuvant to generate antibodies which are useful in vaccines or
 PT immuno:diagnosis
 XX
 Example 1; Fig 1A; 64pp; English.
 XX
 CC Novel recombinant conjugate antibody molecules comprise a monoclonal
 CC antibody specific for a surface structure of antigen presenting
 CC cells (APC), genetically modified to contain at least one antigen
 CC exclusively at one or more preselected sites. The conjugate is capable
 CC of delivering the antigen to APC and eliciting an immune response to
 CC the antigen. The new conjugates are useful as vaccines and are able
 CC to elicit an enhanced immune response without the use of an adjuvant.
 CC In a specific example, a conjugate was constructed using the murine
 CC anti-human class II monoclonal antibody secreted by hybridoma
 CC 44H104. The peptide CLTB36 was chosen as antigen; it consists of
 CC a tandemly linked T and B cell epitope derived from HIV MN strain.
 CC The present sequence encodes the light chain variable region which
 CC was PCR amplified from 44H104 and used in the preparation of a

CC conjugate with antigen CLTB36.
 XX Sequence 387 BP; 90 A; 95 C; 90 G; 112 T; 0 other;
 SQ
 Query Match 23.4%; Score 102; DB 18; Length 387;
 Best Local Similarity 100.0%; Pred. No. 6.6e-42;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DE
 AC AAX00879;
 XX DT 29-MAR-1999 (first entry)
 XX DE Mouse derived RT3 phage antibody light chain pattern C genetic sequence.
 XX KW Catalytic; antibody; phage display; immunizing; phage expression vector;
 KW prodrug; scfv; ss.
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..276
 FT /tag= a
 FT note= "the start and stop codons are not indicated"
 FT
 W09640941-A.
 XX
 PD 05-JAN-1999.
 XX
 PF 14-JUL-1994; 94US-0273146.
 XX
 PR 22-JAN-1993; 93US-0007684.
 PR 14-JUL-1994; 94US-0273146.
 XX
 PA (CHIS/) CHISWELL D.
 PA (DARS/) DARSLEY M J.
 PA (FIZZ/) FITZGERALD K.
 PA (KENT/) KENTEN J H.
 PA (MAR/) MARTIN M T.
 PA (MCCA/) MCCAFFERTY J.
 PA (SMIT/) SMITH R.
 PA (TITM/) TITMAS R C.
 PA (WILL/) WILLIAMS R O.
 XX
 PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH, Smith RC, Williams RO;
 PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;
 XX
 DR WPI: 1999-105036/09.
 DR P-PSDB; AAW93480.
 XX
 PT Production of catalytic antibodies displayed on bacteriophages -
 PT comprises generating a gene library of antibody-derived domains
 PT inserting coding into a phage expression vector and isolating the
 PT catalytic antibodies
 PS Example 4; Fig 11; 117pp; English.
 XX
 CC The invention relates to methods for producing catalytic antibodies
 CC displayed on a phage. The method comprises: (a) generating a gene library
 CC of antibody-derived domains; (b) inserting coding for the domains into a

FT CDS /product= variable region
 FT FT /*tag= C
 FT /product= constant region
 PN EP88994-A.
 XX PD 21-SEP-1983.
 XX PR 10-MAR-1983; 83EP-0001655.
 XX PR 15-MAR-1982; 82US-035414
 PR 05-DEC-1983; 83US-0556551.
 XX PA (SCHE) SCHERING CORP.
 PA (DNAx-) DNAx RES INST.
 XX PI Moore KW, Zaffaroni A;
 XX WPI; 1983-772290/39.
 DR P-PSDB; AAP30251.
 XX PT transformed expression vectors or plasmid(s) - with double
 PT stranded DNA sequence coding only for desired part of polypeptide
 PT chain
 XX PS Example; Page 40-41; 68pp; English.
 CC The pref. vector or plasmid of the invention has a double-stranded
 CC DNA seq. coding for a variable region of a light or heavy chain of
 IGG, or for a variable region of a light or heavy chain of an
 immunoglobulin specific for an enzyme or surface protein. The
 sequence esp. codes for a variable region of a light chain having 95-
 115 AAs or for a variable region of a heavy chain having 110-125 AAs
 esp. including the D region of the heavy chain.
 XX SQ Sequence 450 BP; 108 A; 114 C; 104 G; 124 T; 0 other;

Query Match 23.0%; Score 100; DB 4; Length 450;
 Best Local Similarity 99.3%; Pred. No. 6.8e-41;
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC Example 1; Fig 3; 145pp; English.

Qy 163 TGGCTTCAGGAGAACAGATGGACTATAAAGCCCTGATCTACGCCACATCAGTTA 222
 Db 181 tggttcagggacggacagatggactataaacggctgatctccatccatccatgtta 240
 Qy 223 GGTTCTGGTCCCACAAAGGTGTCAGTGGCAGTAGGTCTGGTGTAGATATTCTCACC 282
 Db 241 gatccctggtgcccaaaaggttcagtggcagcagtgctggcagattatctctcacc 300
 Qy 283 ATCACGAGGCTTGAGTCAGGATTTGGAG 313
 Db 301 atccggcagcttggctaaagatttggag 331
 XX SQ Sequence 535 BP; 126 A; 128 C; 132 G; 149 T; 0 other;

Query Match 21.4%; Score 93; DB 19; Length 535;
 Best Local Similarity 100.0%; Pred. No. 2.3e-37;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 Qy 343 CGGTRACAGTTCGGAGGGGACCRAGCTGGAAATAAACGGGCTGAGCTGCACCAACT 402
 Db 373 ccgtacacgttccggggggggacaaaggctgggataaaacgggtgtgcgtgcaccaact 432
 Qy 403 GTATCCATCTGCCCCACCATCAGTAAGCTGG 435
 Db 433 gtatccatctcccaaccatccatcgaaatggctgg 465
 XX OS Mus sp.

RESULT 7
 AAV20086 ID AAV20086 standard; DNA; 535 BP.
 AC AAV20086;
 XX DT 14-JUL-1998 (first entry)
 DE Consensus DNA sequence of the murine variable light chain region.
 XX
 Mouse: Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adhesion cell adhesion molecule-1; MacCAM-1;
 KW humanised antibody; murine antigen binding; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease; ss.
 XX

RESULT 8
 AAQ90431 ID AAQ90431 standard; DNA; 438 BP.
 XX AC AAQ90431;
 XX

XX haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
 KW tumour; infection; depression; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX WO200021991-A1.
 XX
 PD 20-APR-2000.
 XX PF 15-OCT-1999; 99WO-US24206.
 XX PR 15-OCT-1998; 98US-0104436.
 XX PA (GEMY) GENETICS INST INC.
 XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MR;
 XX DR WPI; 2000-317938/27.
 XX PT Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTS), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
 XX PS claim 1; Page 440; 803pp; English.
 XX
 CC AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (SESTS), isolated from human, mouse, chicken and rat tissue sources. The SESTS can have a range of activities depending on the tissues they were isolated from. The activities include:
 CC chemotactic; proliferative; immunomodulatory; haematopoietic;
 CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
 CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
 CC antiasthmatic; pulmonary; antiulcer; osteopathic; neuroprotective;
 CC nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
 CC anticonvulsant; and antidepressant. The SESTS can be used for gene therapy and in vaccines. The SESTS are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the SESTS. Proteins encoded by the SESTS are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45926 to AAA45931 represent linker variants which are given in the exemplification of the present invention.
 XX Sequence 651 BP; 174 A; 165 C; 151 G; 160 T; 0 other;
 XX
 Query Match 19.5%; Score 85; DB 21; Length 651;
 Best local Similarity 100.0%; Pred. No. 2 6e-33;
 Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 342 TCGTACAGTGGAGGGGGACCAAGCTGAAATAAACGGGTGATGCACCAAC 401
 Db 375 tcggatacgctcgaggggggaccaacggcgatgtgcgaccaa 434
 QY 402 TGTATCCATCTGCCACCATCCAGT 426
 Db 435 tgatccatctccacccatccagt 459
 XX
 RESULT 11
 ID AAT87818
 XX standard; DNA; 652 BP.
 AC AAT87818;
 XX DT 09-DEC-1997 (first entry)
 XX
 Query Match 19.5%; Score 85; DB 17; Length 652;
 Best local Similarity 100.0%; Pred. No. 2 6e-33;
 Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 342 TCGTACAGTGGAGGGGGACCAAGCTGAAATAAACGGGTGATGCACCAAC 401
 Db 202 tcggatacgctcgaggggggaccaacggcgatgtgcgaccaa 341
 QY 402 TGTATCCATCTGCCACCATCCAGT 426
 Db 342 tgatccatctccacccatccagt 366
 XX
 RESULT 12
 ID AAT27849
 XX standard; DNA; 678 BP.
 AC AAA27849;
 XX DT 12-SEP-2000 (first entry)

XX XX
DE WOW-1 Fab light chain DNA.
XX
KW XX
KW -1; Fab; single chain antibody; PAC-1; monoclonal antibody;
KW mouse; integrin; vitronectin receptor alpha_v beta₋₃;
KW drug delivery; gene therapy; ligand mimetic; ss.
XX OS
XX Mus musculus.

XX
FH Key Location/Qualifiers
FT CDS 22..678 /*tag= a
FT /partial

XX
PN WO200034780-A2.
XX
PD 15-JUN-2000.
XX
PF 03-DEC-1999; 99WO-EP09460.
XX
PR 04-DEC-1998; 98US-0110950.
PR 23-JUL-1999; 99US-0145458.
XX
PA (NOVS) NOVARTIS AG.
PA NOVARTIS-ERRINDUNGEN VERW GES MBH.
PA (SCR) SCRIPPS RES INST.
PI Shattil SJ, Nemerow GR, Hato T, Stupack DG, Pampori NA;
XX
DR WPI; 2000-442184/38.
DR P-PSDB; AAY95258.
XX
PT Novel monoclonal antibody that selectively binds activated vitronectin receptor useful for detecting the presence of activated vitronectin receptor in tissue and for delivering therapeutic composition to the tissue.
PT
XX
PS Example 1; Page 15; 42pp; English.

XX
CC The present sequence is that of DNA coding for the light chain (see
CC (AAY95258) of WOW-1 Fab, a novel monovalent ligand-mimetic that
CC selectively binds to activated vitronectin receptor alpha_v beta₋₃.
CC
CC WOW-1 Fab was created by replacing the 19 amino acid heavy chain
complementarity determining region 3 (CDR3) of PAC1 Fab with the 50
amino acid alpha_v integrin-binding domain from adenovirus type 2
penton base protein by splice-overlap PCR (see AAY27830-53). The
modified PAC1 Fab (designated WOW-1) has been expressed as a
His-tagged fusion protein in a Drosophila expression system. WOW-1
is used in a claimed method for detecting the presence of activated
vitronectin receptor alpha_v beta₋₃ in a tissue, and in a claimed
method for delivery of an agent in a therapeutic composition to such
a tissue ex vivo or in vivo, the tissue being selected from
neovascular cells, smooth muscle endothelial cells, arterial cells,
osteoclasts and tumour cells. The agent in the therapeutic
composition is preferably a biologically active compound, especially
a gene, antisense nucleic acid or catalytic nucleic acid (claimed).
Also claimed are nucleic acid expression vectors comprising an
activation cassette encoding a fusion protein comprising an
activated alpha_v beta₋₃ specific ligand, such as the CDR3 domain
or the activated alpha_v beta₋₃ binding domain of Fab WOW-1,
CC operatively linked to a biologically active agent.
XX Sequence 678 BP; 194 A; 171 C; 156 G; 157 T; 0 other;

Query Match 19..5%; score 85; DB 21; length 678;
Best Local Similarity 100.0%; Pred. 2.6e-33;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TCGTACACGTTGGAGGGGGACCAAGCTGGAAATAACGGGGTGTATCTGCACCAAC 401
Db 318 tcggatcaggctcgaggggggaccacgtggaaataaacgggtgtatgtggaccac 377

XX
DE AAQ92503 standard; cDNA; 723 BP.
ID AAQ92503 RESULT 13
XX AC AAQ92503;
XX DT 07-FEB-1996 {first entry}
XX DE Mouse antibody F4-7 light chain variable region coding sequence.
XX KW Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;
KW antibody; immunotolerance; animal; variegated display library;
KW variable region; antigen; immunorecessive; cell surface marker; foetal;
KW cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
KW familial hypercholesterolaemia; binding affinity; ds.
XX OS Mus musculus.

XX
FH Key Location/Qualifiers
FT CDS 67..399 /*tag= a
FT /product= antibody F4-7 light chain variable region

XX
PN WO9515982-A2.
XX PD 15-JUN-1995.
XX PR 08-DEC-1994; 94WO-US14106.
XX PR 06-DEC-1994; 94US-0354400.
PR 08-DEC-1993; 93US-0164022.
XX PA (GENZ) GENZYME CORP.
XX
PI Barsonian G, Copeland DP, Hillhouse D, Johnson T;
XX DR WPI; 1995-224291/29.
DR P-PSDB; AAR75459.
XX
PT Generating new antibodies specific for immunorecessive epitopes
PT by selection from varieated V gene library cloned from
PT immunotolerance derived antibody repertoire, useful in diagnosis,
PT purifcn. and therapy, e.g. of cancer
XX PS Disclosure; Page 80-81; 109pp; English.
CC The coding sequence of the light chain variable region from the mouse
CC antibody F4-7. This sequence was isolated from a variegated display
CC library (VDL) of variable regions derived from a repertoire of
CC antibodies from an immunotolerised animal. The VDL is generated by PCR
CC amplifying the variable regions from the antibody coding sequences using
CC the primers A074153-74. The variable regions, esp the complementarity
CC determining regions (CDR; see AAR75462-93 for examples of CDRs) from the
CC immunotolerant animals' antibodies are used to construct an antibody
CC against a immunorecessive antigen e.g. a cell surface marker on a foetal
CC cancer or stem cell, which can differentiate between variant or related
CC forms of the antigen. The antibodies generated can be used in the
CC diagnosis, e.g. detection of the immunorecessive antigen, or in therapy
CC e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia.
CC The method of production of the antibody allows rapid and sensitive
CC isolation of antibodies that would be difficult to isolate by standard
CC methods. The antibodies produced have greater binding affinity than
CC those produced by combinatorial/hybridoma methods.
XX Sequence 723 BP; 205 A; 195 C; 172 G; 151 T; 0 other;

Query Match 19..5%; Score 85; DB 16; Length 723;

Best Local Similarity 100.0%; Pred. No. 2.6e-33; Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OY 342 TCGCTACAGTTCGGAGGGGACCAACTGGAATAAACCGGCTGATGCCAC 401
 QY 342 TCGCTACAGTTCGGAGGGGACCAACTGGAATAAACCGGCTGATGCCAC 401
 Db 360 tcgtacatcggtggaaataaaacgggtatgcgtgaccac 419
 QY 402 TGTATCCATCTTCCACCATCCAGT 426
 Db 420 tgtatccatcttccaccatccagt 444

RESULT 14
 AAZ61037
 ID AAZ61037 standard; DNA; 738 BP.
 XX
 AC AAZ61037;
 XX
 DT 30-MAY-2000 (first entry)
 XX
 DE Nucleotide sequence of light chain of anti-delta9-desaturase antibody.
 XX
 KW Delta9-desaturase; antibody; transit peptide; passenger protein;
 KW plant cell organelle; maize; stearoyl-ACP-delta9-desaturase;
 KW transgenic plant; light chain; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 37..693 /*tag= a product= "light chain"
 FT
 XX WO20005391-A1.
 XX
 PN 03-FEB-2000.
 XX
 PD 21-JUL-1999; 99WO-US16405.
 XX
 PR 21-JUL-1998; 98US-0093587.
 XX
 PA (DOW) DOW AGROSCIENCES LLC.
 XX
 PI Sukhapinda K, Hasler JM, Petell JK, Strickland JA, Folkerts O;
 PT DR WPI; 2000-182711/16.
 DR P-FSDB; AAY68994.
 XX
 PT Novel nucleic acid construct for down-regulating steady state levels of
 proteins in plant cells, transgenic plants and their progeny
 XX
 PS Claim 21; Page 88-89; 114P; English.
 XX
 CC The present sequence encodes the light chain of a monoclonal antibody
 CC which is directed against a Zea mays (maize) delta9-desaturase. The
 CC present sequence is used to produce the constructs of the invention.
 CC These constructs encode an antibody that can bind a transit peptide
 CC that directs an associated passenger protein to a plant cell organelle.
 CC The transit peptide sequence of the maize stearoyl-ACP-delta9-desaturase
 CC (delta9-desaturase) was determined, and used to produce antibodies of
 CC the invention. These antibodies were produced in transgenic plants of
 CC the invention. The constructs of the invention are useful for producing
 CC antibodies which decrease steady state levels of passenger proteins in
 CC the organelles of plant cells and plants, by binding to the transit
 CC peptide. This results in the production of transgenic plants which
 CC have altered steady state passenger protein levels.
 XX Sequence 738 BP; 203 A; 190 C; 169 G; 168 T; 8 other;

Query Match 19.3%; Score 84; DB 10; Length 639;
 Best Local Similarity 100.0%; Pred. No. 8.2e-33;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OY 342 TCGCTACAGTTCGGAGGGGACCAACTGGAATAAACCGGCTGATGCCAC 401
 Db 333 tcgtacatcggtggaaataaaacgggtatgcgtgaccac 392
 QY 402 TGTATCCATCTTCCACCATCCAGT 426
 Db 393 tgtatccatcttccaccatccagt 417

RESULT 15
 AA91657
 ID AA91657 standard; DNA; 639 BP.
 XX
 AC AA91657;
 XX
 DT 14-MAR-1990 (first entry)
 XX
 DE Chimeric antibody light chain variable region.
 XX
 OS Mus.
 XX
 KW KSL1/4; chimeric antibody; light chain variable region;
 KW Beavers LS, Bumol TF, Gadski RA, Weigel BJ;
 XX
 PR 18-APR-1989; 89EP-0303814.
 XX
 PR 21-APR-1988; 88US-0184522.
 XX
 PA (ELIL) ELI LILLY AND CO.
 XX
 PI Beavers LS, Bumol TF, Gadski RA, Weigel BJ;
 XX
 DR WPI; 1989-31203/43.
 DR P-PSDB; AAP93035.
 XX
 PT Recombinant DNA cpds. producing antibodies - monoclonal and
 PT chimeric derived from monoclonal antibody KSL1/4.
 XX
 PS Claim 2; page 49; 89PP; English.
 XX
 CC The DNA encodes the light chain of monoclonal antibody KSL1/4, used to
 CC construct mouse/human chimeric antibodies. KSL1/4 is a murine antibody
 CC which binds to surface antigens on adenocarcinoma cells and the use of
 CC human C regions avoids immunological problems during treatment.
 XX
 SQ Sequence 639 BP; 174 A; 175 C; 149 G; 141 T; 0 other;

Query Match 19.3%; Score 84; DB 10; Length 639;
 Best Local Similarity 100.0%; Pred. No. 8.2e-33;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OY 343 CGGTACAGTTCGGAGGGGACCAACTGGAATAAACCGGCTGATGCCAC 402
 Db 280 cggtagatcggtggaaataaaacgggtatgcgtgaccac 339
 QY 403 GTATCCATCTTCCACCATCCAGT 426
 Db 340 gtatccatcttccaccatccagt 363

Search completed: February 21, 2002, 04:28:51
 Job time: 28000 sec

Thu Feb 21 13:44:40 2002

us-08-836-455-1.oli.rng

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2002, 20:39:26 ; Search time 2034.98 Seconds
(without alignments)
2297.032 Million cell updates/sec

Title: US-08-836-455-1

Perfect score: 435

Sequence: 1 ATGGGGCCCTGCAGAT.....CACCATCCAGTAAGCTGGG 435

Scoring table: ORIGO_NUC
gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : EST:*

- 1: em_gss_profun:*
- 2: em_esthun:*
- 3: em_estin:*
- 4: em_estom:*
- 5: em_estpl:*
- 6: em_estba:*
- 7: em_estro:*
- 8: em_estov:*
- 9: em_htc:*
- 10: gb_est1:*
- 11: gb_est2:*
- 12: gb_htc:*
- 13: gb_gss:*
- 14: em_gss_fun:*
- 15: em_gss_hum:*
- 16: em_gss_inv:*
- 17: em_gss_pln:*
- 18: em_gss_pro:*
- 19: em_gss_rnd:*
- 20: em_gss_vrt:*
- 21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	87	20.0	594	10 BE309592
2	85	19.5	725	11 BG963055
3	85	19.5	891	11 BF579422
4	85	19.5	906	11 BF785914
5	84	19.3	975	11 BG961850
6	83	19.1	750	11 BG955050
7	81	18.6	630	11 BF138788
8	81	18.6	707	11 BI220555
9	79	18.2	712	11 BI100311
10	79	18.2	778	11 BG964076
11	79	18.2	798	11 BG985118
12	75	17.2	944	11 BF687485

ALIGNMENTS

		/dev_stage="7 months"
		/Lab_host=DH10B"
Query Match	19.5%; Score 85; DB 11; Length 891;	/note="Organism: mammary; Vector: PCMV-SPOR6; Site_1: Sali; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Best Local Similarity	100.0%; Pred. No. 6.6e-34; Mismatches 0; Indels 0; Gaps 0;	Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Matches	85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Library constructed by Life Technologies. Investigators providing samples: Lothar Henninghausen/Robbin Humphries,
QY	342 TCCGTACAGGTCGGAGGGGGACCAAGCTGGAAATAAACGGGCATGCTGCACCAAC 401	NIH" NIH" house mouse.
BASE COUNT	158 a 149 c 143 g 144 t	
ORIGIN		
RESULT	3	
DB	372 TCCGTACACGTTGGGGGGACCTGSGAATAAACGGGCTGATGCTGCCACCAAC 431	
LOCUS	BF579422 891 bp mRNA EST	12-DEC-2000
DEFINITION	60209383f1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208144 5'	
ACCESSION	BF579422	
VERSION	BF579422.1 GI:11653134	
KEYWORD	EST	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	2	
DB	372 TCCGTACATTCGGGACCAAGCTGGAAATAAACGGGTGATCTGACCA 399	
LOCUS	BG963055 725 bp mRNA EST	12-JUN-2001
DEFINITION	602828068f1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982825 5'	
ACCESSION	BG963055	
VERSION	BG963055.1 GI:14350692	
KEYWORD	EST	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 725)	
AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: http://image.lilnl.gov Plate: LILAM9772 row: a column: 09 High quality sequence stop: 711. Location/Qualifiers	
FEATURES	Source	
	/organism="Mus musculus" /strain="FVB/N" /db_xref=taxon:10090" /clone="IMAGE:4208144" /clone_id="NCI_CGAP_Co24" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: colon; Vector: PCMV-SPOR6; Site_1: NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	246 a 226 c 204 g 215 t	
ORIGIN		
RESULT	4	
DB	372 TCCGTACATTCGGGACCAAGCTGGAAATAAACGGGTGATCTGACCA 401	
LOCUS	BF785914 906 bp mRNA EST	12-JAN-2001
DEFINITION	60211254f1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240762	
ACCESSION	BF785914	
VERSION	BF785914.1 GI:12090950	
KEYWORD	EST	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	4	
DB	372 TCCGTACACGTTGGGGGGACCAAGCTGGAAATAAACGGGCTGATGCTGCCACCAAC 431	
LOCUS	BF785914	
DEFINITION	60211254f1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240762	
ACCESSION	BF785914	
VERSION	BF785914.1 GI:12090950	
KEYWORD	EST	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
FEATURES	source	
	1. .725 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:982825" /clone_id="NCI_CGAP_Co24" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: colon; Vector: PCMV-SPOR6; Site_1: NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	246 a 226 c 204 g 215 t	
ORIGIN		
RESULT	4	
DB	372 TCCGTACATTCGGGACCAAGCTGGAAATAAACGGGTGATCTGACCA 401	
LOCUS	BF785914	
DEFINITION	60211254f1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240762	
ACCESSION	BF785914	
VERSION	BF785914.1 GI:12090950	
KEYWORD	EST	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
FEATURES	source	
	1. .725 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:982825" /clone_id="NCI_CGAP_Co24" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: colon; Vector: PCMV-SPOR6; Site_1: NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	246 a 226 c 204 g 215 t	
ORIGIN		
RESULT	4	
DB	372 TCCGTACACGTTGGGGGGACCAAGCTGGAAATAAACGGGCTGATGCTGCCACCAAC 431	
LOCUS	BF785914	
DEFINITION	60211254f1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240762	
ACCESSION	BF785914	
VERSION	BF785914.1 GI:12090950	
KEYWORD	EST	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
FEATURES	source	
	1. .725 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:982825" /clone_id="NCI_CGAP_Co24" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: colon; Vector: PCMV-SPOR6; Site_1: NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	246 a 226 c 204 g 215 t	
ORIGIN		
RESULT	4	
DB	372 TCCGTACACGTTGGGGGGACCAAGCTGGAAATAAACGGGCTGATGCTGCCACCAAC 431	
LOCUS	BF785914	
DEFINITION	60211254f1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240762	
ACCESSION	BF785914	
VERSION	BF785914.1 GI:12090950	
KEYWORD	EST	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

	FEATURES SOURCE	FEATURES SOURCE	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Location/Qualifiers 1. .975	
AUTHORS	1 (bases 1 to 906) NIH-MGC http://mgc.ncbi.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	/organism="Mus musculus"	
TITLE	Contact: Robert Strausberg, Ph.D.	/strain="FVB/N"	
JOURNAL	Email: cggaps-r@mail.nih.gov	/db_xref="taxon:10090"	
COMMENT	Tissue Procurement: Jeffrey E. Green, M.D.	/clone="IMAGE:4981443"	
	CDNA Library Preparation: Life Technologies, Inc.	/clone_1.lib="NCI_CGAP_Kid14"	
	DNA Sequencing by: Incyte Genomics, Inc.	/lab_host="DH10B (T1 phage-resistant)"	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	/note="Organ: Colon; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr."	
	http://image.llnl.gov	Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	Plate: LLM0855 row: p column: 11	202 a 264 C 210 g 213 t	
ORIGIN	High quality sequence stop: 718.	243 a 232 C 237 g 194 t	
FEATURES SOURCE	Location/Qualifiers 1. .906		
	/organism="Mus musculus"		
	/strain="FVB/N"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:4240762"		
	/clone_1.lib="NCI_CGAP_Kid14"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/note="Organ: kidney; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr."		
	Average insert size 1.7 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. "		
BASE COUNT			
ORIGIN			
Query Match	19.5%; Score 85; DB 11; Length 906;	Query Match 19.3%; Score 84; DB 11; Length 975;	
Best Local Similarity	100.0%; Pred. No. 6.7e-34;	Best Local Similarity 100.0%; Pred. No. 2.3e-33;	
Matches	85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	342 TCCGTACAGCTTCGGAGGGGGACCAAGTGAAATAAACGGGCTGATGCTGCCAAC 401	Qy 343 CGGTACACGTTGGAGGGGGACCAAGTGAAATAAACGGGCTGATGCTGCCAAC 402	
Db	371 TCCGTACAGCTTCGGAGGGGGACCAAGTGAAATAAACGGGCTGATGCTGCCAAC 430	Db 363 CGGTACACGTTGGAGGGGGACCAAGTGAAATAAACGGGCTGATGCTGCCAAC 422	
Qy	402 TGTATCCACCTTCCACCATCCTACT 425	Qy 403 GTATCCATCTCCACCATCCTACT 426	
Db	431 TGTATCCACCTTCCACCATCCTACT 455	Db 423 GTATCCATCTCCACCATCCTACT 446	
RESULT		RESULT	
LOCUS	BG965050	LOCUS	BG965050
DEFINITION	602829112F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983962 5', mRNA sequence.	DEFINITION	750 bp mRNA
ACCESSION	BG965050	ACCESSION	BG965050.1 GI:14352687
VERSION		VERSION	
KEYWORDS		KEYWORDS	
SOURCE		SOURCE	
ORGANISM	Mus musculus	ORGANISM	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 750) NIH-MGC http://mgc.ncbi.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	AUTHORS	1 (bases 1 to 750) NIH-MGC http://mgc.ncbi.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
TITLE	Contact: Robert Strausberg, Ph.D.	TITLE	Contact: Robert Strausberg, Ph.D.
JOURNAL	Email: cggaps-r@mail.nih.gov	JOURNAL	Email: cggaps-r@mail.nih.gov
COMMENT	Tissue Procurement: Jeffrey E. Green, M.D.	COMMENT	CDNA Library Preparation: Life Technologies, Inc.
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov		http://image.llnl.gov
	Plate: LLM0989 row: g column: 03		Plate: LLM0989 row: g column: 03
	High quality sequence stop: 748.		High quality sequence stop: 748.
FEATURES SOURCE	Location/Qualifiers 1. .750	FEATURES SOURCE	Location/Qualifiers 1. .750
	/organism="Mus musculus"		/organism="Mus musculus"
	/strain="FVB/N"		/strain="FVB/N"
	/db_xref="taxon:10090"		/db_xref="taxon:10090"
	/clone="IMAGE:4983962"		/clone="IMAGE:4983962"
	/clone_1.lib="NCI_CGAP_Co24"		/clone_1.lib="NCI_CGAP_Co24"
	/lab_host="DH10B (T1 phage-resistant)"		/lab_host="DH10B (T1 phage-resistant)"
	/note="Organ: Colon; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr."		/note="Organ: Colon; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr."
BASE COUNT	202 a 193 C 181 g 174 t	BASE COUNT	19.1%; Score 83; DB 11; Length 750;
ORIGIN	High quality sequence stop: 743.	Query Match	19.1%; Score 83; DB 11; Length 750;

			Best Local Similarity 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DEFINITION 60299314F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5149563 5', mRNA sequence.
Oy	344	CCTACAGCTGGAGGGGACAAAGCTGAAATAAACCGGGCTATGCCGCAACTG 403	LOCUS BT100311	VERSION BT100311
Db	386	CGTACAGCTGGAGGGGACAAAGCTGAAATAAACCGGGCTATGCCGCAACTG 445	DEFINITION 602885776F1 NCI_CGAP_Kid14 Mus musculus EST	KEYWORD EST.
Oy	404	TATCCATCTCCACCATCCAGT 426	ACCESSION BI100311.1	VERSION BI100311.1
Db	446	TATCCATCTCCACCATCCAGT 468	DEFINITION 602885776F1 NCI_CGAP_Kid14 Mus musculus EST	KEYWORD EST.
RESULT	7		SOURCE house mouse.	ORGANISM Mus musculus
LOCUS	BT138788	630 bp mRNA	COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DEFINITION	601780387F1 NCI_CGAP_Lu30	Mus musculus cDNA clone IMAGE:4008404 5', mRNA sequence.	REFERENCE 1 (bases 1 to 707)	AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
ACCESSION	BT138788	EST	TITLE National Institutes of Health, Mammalian Gene Collection (MGC)	JOURNAL Unpublished (1999)
VERSION	BT138788.1	GI:10977828	COMMENT Contact: Robert Strausberg, Ph.D.	CDNA Library Preparation: Life Technologies, Inc.
KEYWORDS		EST.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	DNA Sequencing by: Incyte Genomics, Inc.
COMMENT		house mouse.	Plate: LLAM1361 row: k column: 04	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
ORGANISM	Mus musculus		High quality sequence stop: 707.	CDNA Library Preparation: Life Technologies, Inc.
REFERENCE	1 (bases 1 to 630)		Location/Qualifiers 1. .707	Tissue Procurement: Life Technologies, Inc.
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		/organism="Mus musculus"	CDNA Library Preparation: Life Technologies, Inc.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		/strain="C57/B6"	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
JOURNAL	Unpublished (1999)		/db_xref="taxon:10990"	CDNA Library Preparation: Life Technologies, Inc.
Contact	Robert Strausberg, Ph.D.		/clone="IMAGE:5149563"	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Email:	crapsb@email.nih.gov		/clone_id="NCI_CGAP_Mam5"	CDNA Library Preparation: Life Technologies, Inc.
Tissue Procurement	Gilbert Smith, Ph.D.		/tissue_type="tumor, gross tissue"	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
CDNA Library Preparation	Life Technologies, Inc.		/dev_start="7 months"	CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by	The I.M.A.G.E. Consortium (LLNL)		/lab_host="DH10B"	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
DNA Sequencing by	Incyte Genomics, Inc.		/note="Organ: mammary; Vector: pcMV-SPORT6; Site_1: Sali; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"	CDNA Library Preparation: Life Technologies, Inc.
Clone distribution	NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			CDNA Library Preparation: Life Technologies, Inc.
NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov				CDNA Library Preparation: Life Technologies, Inc.
Plate	LLAM9242	row: n column: 21		
High quality sequence stop	628.			
FEATURES	source			
source	1..630			
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/strain="CZECH II"				
/db_xref="taxon:10990"				
/clone="IMAGE:4008404"				
/clone_id="NCI_CGAP_Lu30"				
/tissue_type="tumor, metastatic to mammary"				
/lab_host="DH10B"				
/note="Organ: lung; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: SalI; Transgenic model: WNT1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"				
Investigator providing samples	Gilbert Smith, NIH			
BASE COUNT	198 a 171 c 172 g 166 t			
ORIGIN				
Query Match	18.6%; Score 81; DB 11; Length 630;			
Best Local Similarity	100.0%; Pred. No. 8.4e-32;			
Matches	81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
LOCUS	BT100311			
DEFINITION	602885776F1 NCI_CGAP_Kid14 Mus musculus EST			
ACCESSION	BI100311			
VERSION	BI100311.1			
KEYWORDS	EST.			
COMMENT	house mouse.			
ORGANISM	Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 {bases 1 to 712}			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
Contact	Robert Strausberg, Ph.D.			
RESULT	9			
LOCUS	BT100311			
DEFINITION	602885776F1 NCI_CGAP_Kid14 Mus musculus EST			
ACCESSION	BI100311			
VERSION	BI100311.1			
KEYWORDS	EST.			
COMMENT	house mouse.			
ORGANISM	Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 {bases 1 to 712}			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
Contact	Robert Strausberg, Ph.D.			
RESULT	8			
LOCUS	BT1250555			
DEFINITION	602885776F1 NCI_CGAP_Kid14 Mus musculus EST			
ACCESSION	BI1250555			
VERSION	BI1250555.1			
KEYWORDS	EST.			
COMMENT	17-JUL-2001			

Best Local Similarity 100.0%; Pred. No. 2e-24; Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 /db_xref="Taxon:10090"
 /clone="IMAGE:4965159"
 /clone.lib="NCI_CGAP_Co24"
 /lab_host="DH10B" (T1 phage-resistant)"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 210 a 236 c 169 g 178 t
 ORIGIN

Query Match 16.8%; Score 73; DB 11; Length 793;
 Best Local Similarity 100.0%; Pred. No. 1.4e-27;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 Db 398 GGGACCACTGGAGAAACACCGCCTATGCCAC 419
 Qy 420 ATCCAGT 426
 Db 458 ATCCAGT 464

RESULT 15
 BI04783 BI04783 532 bp mRNA EST 26-JUN-2001
 DEFINITION 602891329F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:503622 5',
 mRNA sequence.

ACCESSION BI04783
 VERSION BI04783.1 GI:14555676
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 532)
 NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS NIH-MGC
 TITLE Unpublished (1999)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Contact: Robert Strasberg, Ph.D.
 Email: cgbabs1@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://imaged.lnl.gov
 Plate: LNL1101 row: i column: 07
 High quality sequence stop: 532.
 FEATURES location/Qualifiers
 source 1. .532

/organism="Mus musculus"
 /strain="CZUCH II (fetal)"
 /db_xref="Taxon:10090"
 /clone="IMAGE:5036622"
 /clone.lib="NCI_CGAP_Lu29"
 /tissue_type="spontaneous tumor, metastatic to mammary."
 /stem_cell_origin"
 /lab_host="DH10B"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"
 BASE COUNT 139 a 148 c 113 g 132 t
 ORIGIN
 Query Match 15.4%; Score 67; DB 11; Length 532;

Search completed: February 21, 2002, 04:00:25
 Job time: 26459 sec

Thu Feb 21 13:44:41 2002

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